

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 12:23:23 ; Search time 106.32 Seconds
(without alignments)
399.753 Million cell updates/sec

Title: US-09-852-659-85

Perfect score: 613

Sequence: 1 MRLMLFTAILAFSLAQSGF.....DVNQENVPSGILKYPPRAE 121

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3516493 seqs, 351254056 residues

Total number of hits satisfying chosen parameters: 3516493

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_Main:*

- 1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
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- 25: /cgn2_6/ptodata/2/paa/US60_MERGED_COMB.pep1.*
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- 27: /cgn2_6/ptodata/2/paa/US09_MERGED_COMB.pep2.*
- 28: /cgn2_6/ptodata/2/paa/US09_MERGED_COMB.pep1.*
- 29: /cgn2_6/ptodata/2/paa/US08_MERGED_COMB.pep1.*
- 30: /cgn2_6/ptodata/2/paa/US07_MERGED_COMB.pep1.*
- 31: /cgn2_6/ptodata/2/paa/US06_MERGED_COMB.pep1.*
- 32: /cgn2_6/ptodata/2/paa/PCT_MERGED_COMB.pep1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	610	99.5	121 14	US-09-086-078-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-086-078-2
; Sequence 2, Application US/09086078
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NEUROKININ B PRECURSORS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics
; STREET: 1201 Eastlake Ave. E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,078
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

2	610	99.5	121	15	US-09-111-901-2	Sequence 2, Appli
3	610	99.5	121	15	US-09-152-060-68	Sequence 68, Appl
4	610	99.5	121	22	US-09-852-659-68	Sequence 68, Appl
5	610	99.5	121	22	US-09-852-797-68	Sequence 68, Appl
6	610	99.5	121	22	US-09-853-161-68	Sequence 68, Appl
7	610	99.5	121	26	US-10-058-993-68	Sequence 68, Appl
8	610	99.5	137	1	PCT-US01-03800A-2248	Sequence 2248, Ap
9	609	99.3	121	15	US-09-152-060-85	Sequence 85, Appl
10	609	99.3	121	22	US-09-852-659-85	Sequence 85, Appl
11	609	99.3	121	22	US-09-852-797-85	Sequence 85, Appl
12	609	99.3	121	22	US-09-853-161-85	Sequence 85, Appl
13	609	99.3	121	26	US-10-058-993-85	Sequence 85, Appl
14	592.5	96.7	122	12	US-08-879-995-1	Sequence 1, Appli
15	592.5	96.7	122	18	US-09-437-860-1	Sequence 1, Appli
16	539	87.9	108	22	US-09-834-366-13657	Sequence 13657, A
17	539	87.9	108	24	US-60-197-873-13657	Sequence 13657, A
18	487	79.4	135	21	US-09-709-238-359	Sequence 359, App
19	487	79.4	135	23	US-09-929-404-357	Sequence 357, App
20	487	79.4	135	23	US-09-941-992-359	Sequence 359, App
21	487	79.4	135	26	US-10-052-586-444	Sequence 444, App
22	487	79.4	135	26	US-10-081-056-170	Sequence 170, App
23	487	79.4	135	27	US-09-989-723-359	Sequence 359, App
24	487	79.4	135	27	US-09-989-724-359	Sequence 359, App
25	487	79.4	135	27	US-09-989-730-359	Sequence 359, App
26	487	79.4	135	27	US-09-990-436-359	Sequence 359, App
27	487	79.4	135	27	US-09-990-444-359	Sequence 359, App
28	487	79.4	135	27	US-09-989-721-359	Sequence 359, App
29	487	79.4	135	27	US-09-989-722-359	Sequence 359, App
30	487	79.4	135	27	US-09-989-725-359	Sequence 359, App
31	487	79.4	135	27	US-09-989-726-359	Sequence 359, App
32	487	79.4	135	27	US-09-989-727-359	Sequence 359, App
33	487	79.4	135	27	US-09-989-728-359	Sequence 359, App
34	487	79.4	135	27	US-09-989-731-359	Sequence 359, App
35	487	79.4	135	27	US-09-989-732-359	Sequence 359, App
36	487	79.4	135	27	US-09-989-733-359	Sequence 359, App
37	487	79.4	135	27	US-09-989-734-359	Sequence 359, App
38	487	79.4	135	27	US-09-990-437-359	Sequence 359, App
39	487	79.4	135	27	US-09-990-438-359	Sequence 359, App
40	487	79.4	135	27	US-09-990-440-359	Sequence 359, App
41	487	79.4	135	27	US-09-989-279-359	Sequence 359, App
42	487	79.4	135	27	US-09-989-735-359	Sequence 359, App
43	487	79.4	135	27	US-09-990-439-359	Sequence 359, App
44	487	79.4	135	27	US-09-990-562-359	Sequence 359, App
45	487	79.4	135	27	US-09-997-529-359	Sequence 359, App

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lingenfelter, Susan E
REGISTRATION NUMBER: 41,156
REFERENCE/DOCKET NUMBER: 97-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6675
TELEFAX: 206-442-6678
TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-086-078-2

Query Match 99.5%; Score 610; DB 14; Length 121;
Best Local Similarity 98.3%; Pred. No. 1.5e-62;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPOEEVVGGRSKRDPDLYQLLQRLFKSHSLEGL 60
DB 1 MRIMLLFTAILAFSLAQSGAVCKEPOEEVVGGRSKRDPDLYQLLQRLFKSHSLEGL 60
QY 61 LKALSQXSTDPKSTSPKRDMDHDFVGMGRKSVQPDSDTDVNOENVPFSGILKYPPRA 120
DB 61 LKALSQASTDPKSTSPKRDMDHDFVGLMGKRSVQPDSDTDVNOENVPFSGILKYPPRA 120
QY 121 E 121
DB 121 E 121

RESULT 2
US-09-111-901-2
Sequence 2, Application US/09111901
GENERAL INFORMATION:
APPLICANT: DUCKWORTH, DAVID
APPLICANT: HASTINGS, GREGG
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,901
FILING DATE: 08-JULY-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 97305215.2
FILING DATE: 14-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-30331
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701

TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-111-901-2

Query Match 99.5%; Score 610; DB 15; Length 121;
Best Local Similarity 98.3%; Pred. No. 1.5e-62;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPOEEVVGGRSKRDPDLYQLLQRLFKSHSLEGL 60
DB 1 MRIMLLFTAILAFSLAQSGAVCKEPOEEVVGGRSKRDPDLYQLLQRLFKSHSLEGL 60
QY 61 LKALSQXSTDPKSTSPKRDMDHDFVGMGRKSVQPDSDTDVNOENVPFSGILKYPPRA 120
DB 61 LKALSQASTDPKSTSPKRDMDHDFVGLMGKRSVQPDSDTDVNOENVPFSGILKYPPRA 120
QY 121 E 121
DB 121 E 121

RESULT 3
US-09-152-060-68
Sequence 68, Application US/09152060
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P1 US
CURRENT APPLICATION NUMBER: US/09/152,060
EARLIER FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: PCT/US98/04858
EARLIER FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/050,934
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,357
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/057,765
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 68
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapiens
US-09-152-060-68

Query Match 99.5%; Score 610; DB 15; Length 121;
Best Local Similarity 98.3%; Pred. No. 1.5e-62;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPOEEVVGGRSKRDPDLYQLLQRLFKSHSLEGL 60
DB 1 MRIMLLFTAILAFSLAQSGAVCKEPOEEVVGGRSKRDPDLYQLLQRLFKSHSLEGL 60

Qy	61	LKALSQASTDPKESTPEKRDMDHDFVVGXMGKRSVQDPSPTDVNQENVSFGLKYPPRA	120
D _b	61	LKALSQASTDPKESTPEKRDMDHDFVGLMGKRSVQDPSPTDVNQENVSFGLKYPPRA	120
Qy	121	E 121	
D _b	121	E 121	

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RESULT 4
US-09-852-659-68
; Sequence 68, Application US/09852659
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659-68

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	Query Match	99.5%;	Score 610;	DB 22;	Length 121;	
	Best Local Similarity	98.3%;	Pred. No. 1.5e-62;			
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Dd	1 MRIMLLFTALFLAQSFGAVCKEPOEEVVPGGGRSKRDPDLQLQLRLFKSHSSLEGL	60				
QY	61 LKALSQXSTDPKESTSPKKRDMHDFVGVXMGKRVSQDPSPTDVNQENVPFSGILKYPPRA	120				
Dd	61 LKALSQAOSTDPKESTSPKKRDMHDFVGLMKGKRVSQDPSPTDVNQENVPFSGILKYPPRA	120				
QY	121 E 121					
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Dd	121 E 121					

RESULT 5
US-09-852-797-68
; Sequence 68, Application US/09852797
; GENERAL INFORMATION:

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: APPLICANT: Rosen et al.
: TITLE OF INVENTION: 28 Human Secreted Proteins
: FILE REFERENCE: P2003P2
: CURRENT APPLICATION NUMBER: US/09/852,797
: CURRENT FILING DATE: 2001-05-11
: PRIORITY APPLICATION NUMBER: 60/265,583
: PRIORITY FILING DATE: 2001-02-02
: PRIORITY APPLICATION NUMBER: 09/152,060
: PRIORITY FILING DATE: 1998-09-11
: PRIORITY APPLICATION NUMBER: PCT/US98/04858
: PRIORITY FILING DATE: 1998-03-12
: PRIORITY APPLICATION NUMBER: 60/040,762
: PRIORITY FILING DATE: 1997-03-14
: PRIORITY APPLICATION NUMBER: 60/040,710
: PRIORITY FILING DATE: 1997-03-14
: PRIORITY APPLICATION NUMBER: 60/050,934
: PRIORITY FILING DATE: 1997-05-30
: PRIORITY APPLICATION NUMBER: 60/048,100
: PRIORITY FILING DATE: 1997-05-30
: PRIORITY APPLICATION NUMBER: 60/048,357
: PRIORITY FILING DATE: 1997-05-30
: PRIORITY APPLICATION NUMBER: 60/048,189
: PRIORITY FILING DATE: 1997-05-30
: PRIORITY APPLICATION NUMBER: 60/057,765
: PRIORITY FILING DATE: 1997-09-05
: PRIORITY APPLICATION NUMBER: 60/048,970
: PRIORITY FILING DATE: 1997-06-06
: PRIORITY APPLICATION NUMBER: 60/068,368
: PRIORITY FILING DATE: 1997-12-19
: NUMBER OF SEQ ID NOS: 118
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 68
: LENGTH: 121
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-852,797-68

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[illegible]

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RESULT 6
US-09-853-161-68
Sequence 68, Application US/09853161
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P3
CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
PRIORITY APPLICATION NUMBER: 60/265,583
PRIORITY FILING DATE: 2001-02-02
PRIORITY APPLICATION NUMBER: 09/152,060
PRIORITY FILING DATE: 1998-09-11
PRIORITY APPLICATION NUMBER: PCT/US98/04858
PRIORITY FILING DATE: 1998-03-12
PRIORITY APPLICATION NUMBER: 60/040,762
PRIORITY FILING DATE: 1997-03-14
PRIORITY APPLICATION NUMBER: 60/040,710

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, PRIOR FILING DATE: 1997-03-14
, PRIOR APPLICATION NUMBER: 60/050,934
, PRIOR FILING DATE: 1997-05-30
, PRIOR APPLICATION NUMBER: 60/048,100
, PRIOR FILING DATE: 1997-05-30
, PRIOR APPLICATION NUMBER: 60/048,357
, PRIOR FILING DATE: 1997-05-30
, PRIOR APPLICATION NUMBER: 60/048,189
, PRIOR FILING DATE: 1997-05-30
, PRIOR APPLICATION NUMBER: 60/057,765
, PRIOR FILING DATE: 1997-09-05
, PRIOR APPLICATION NUMBER: 60/048,970
, PRIOR FILING DATE: 1997-06-06
, PRIOR APPLICATION NUMBER: 60/068,368
, PRIOR FILING DATE: 1997-12-19
, NUMBER OF SEQ ID NOS: 118
, SOFTWARE: PatentIn Ver. 2.0
, SEQ ID NO 68
, LENGTH: 121
, TYPE: PRT
, ORGANISM: Homo sapiens
, US-09-853,161-68

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[illegible]

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RESULT 7
US-10-058-993-68
; Sequence 68, Application US/10058993
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189

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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: prt
; ORGANISM: Homo sapiens
; US-10-058-993-68

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	Query Match	99.5%;	Score 610;	DB 26;	Length 121;
	Best Local Similarity	98.3%;	Pred. No. 1.5e-62;		
	Matches 119;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1 MRIMLLFTAILAFSLAQSFGAVCKEPEOEVVPGGSRKRDPDQLYQLLQRLFKSHSSLEGL	60			
Dd	1 MRIMLLFTAILAFSLAQSFGAVCKEPEOEVVPGGSRKRDPDQLYQLLQRLFKSHSSLEGL	60			
Qy	61 LKALSQASTDPKESTSPDKRDMHDFVFXGMGRSQVDPSPTDVNQNVNVPFSGILKYPPRA	120			
Dd	61 LKALSQASTDPKESTSPDKRDMHDFVFXGMGRSQVDPSPTDVNQNVNVPFSGILKYPPRA	120			
Qy	121 E 121				
Dd	121 E 121				

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RESULT      8
PCT-US01-03800A-2248
; Sequence 2248, Application PC/TUS0103800A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: PCT/US01/03800A
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2248
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-03800A-2248

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	Query Match	99.5%	Score 610;	DB 1;	Length 137;
	Best Local Similarity	98.3%;	Pred. No. 1.8e-62;		
	Matches 119;	Conservative	0;	Mismatches 2;	Indels 0;
	Gaps				
Qy	1	MRIMLLFTAILAFSLAQSGFAGVCKPEQEEVPPGGGRSKRDPDLYQLLQRLFKSHSSLEGL	60		
Db	17	MRIMLLFTAILAFSLAQSGFAGVCKPEQEEVPPGGGRSKRDPDLYQLLQRLFKSHSSLEGL	76		
Qy	61	LKALQSXTDPDKESTSPKRDMDHDFVGMGKRSPQDPSPTDVNQENVPVSFGILKYPPRA	120		
Db	77	LKALQSXTDPDKESTSPKRDMDHDFVGMGKRSPQDPSPTDVNQENVPVSFGILKYPPRA	136		
Qy	121	E 121			
		+			
Db	137	E 137			


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RESULT 9
US-09-152-060-85
; Sequence 85, Application US/09152060
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (89)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-152-060-85

Query Match          99.3%; Score 609; DB 15; Length 121;
Best Local Similarity 100.0%; Pred. No. 2e-62;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 MRTLMLFTAILAFSLAQSGAVCKEPEVPGGSRKRDPLDYQLLQRLFKSHSSLEGL 60
    |||||||
Db 1 MRTLMLFTAILAFSLAQSGAVCKEPEVPGGSRKRDPLDYQLLQRLFKSHSSLEGL 60
    |||||||
QY 61 LKALSOXSTDPKRESTSPKRDHMFVCGXMGKRSVQDPDPTDVNQENVPFGLIKYPPRA 120
    |||||||
Db 61 LKALSOXSTDPKRESTSPKRDHMFVCGXMGKRSVQDPDPTDVNQENVPFGLIKYPPRA 120
    |||||||
QY 121 E 121
    |
Db 121 E 121

RESULT 10
US-09-852-659-85
; Sequence 85, Application US/09852659
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583

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;; PRIOR APPLICATION NUMBER: 60/040,710
;; PRIOR FILING DATE: 1997-03-14
;; PRIOR APPLICATION NUMBER: 60/050,934
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: 60/048,100
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: 60/048,357
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: 60/048,189
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: 60/057,765
;; PRIOR FILING DATE: 1997-09-05
;; PRIOR APPLICATION NUMBER: 60/048,970
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/068,368
;; PRIOR FILING DATE: 1997-12-19
;; NUMBER OF SEQ ID NOS: 118
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 85
;; LENGTH: 121
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (67)
;; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (89)
;; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-852-797-85

Query Match 99.3%; Score 609; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 2e-62;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRIMLLFTAILAFSLAQSGAVCKEPEQEEVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSGAVCKEPEQEEVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
QY 61 LKALSOXSTDPKESTPEKRDMDHDFVGMGKRSVQPDSDTDVNOENVPVSFGILKYPPRA 120
Db 61 LKALSOXSTDPKESTPEKRDMDHDFVGMGKRSVQPDSDTDVNOENVPVSFGILKYPPRA 120
QY 121 E 121
Db 121 E 121

RESULT 12
US-09-853-161-85
; Sequence 85, Application US/09853161
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357

;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: 60/048,189
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: 60/057,765
;; PRIOR FILING DATE: 1997-09-05
;; PRIOR APPLICATION NUMBER: 60/048,970
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/068,368
;; PRIOR FILING DATE: 1997-12-19
;; NUMBER OF SEQ ID NOS: 118
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 85
;; LENGTH: 121
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (67)
;; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (89)
;; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-853-161-85

Query Match 99.3%; Score 609; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 2e-62;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRIMLLFTAILAFSLAQSGAVCKEPEQEEVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSGAVCKEPEQEEVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
QY 61 LKALSOXSTDPKESTPEKRDMDHDFVGMGKRSVQPDSDTDVNOENVPVSFGILKYPPRA 120
Db 61 LKALSOXSTDPKESTPEKRDMDHDFVGMGKRSVQPDSDTDVNOENVPVSFGILKYPPRA 120
QY 121 E 121
Db 121 E 121

RESULT 13
US-10-058-993-85
; Sequence 85, Application US/10058993
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: 60/048,189
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: 60/048,357
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: 60/040,710
;; PRIOR FILING DATE: 1997-03-14
;; PRIOR APPLICATION NUMBER: 60/040,762
;; PRIOR FILING DATE: 1997-03-14
;; NUMBER OF SEQ ID NOS: 122
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 85
;; LENGTH: 121
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (67)
;; OTHER INFORMATION: Xaa equals any amino acid
;; NAME/KEY: SITE
;; LOCATION: (89)
;; OTHER INFORMATION: Xaa equals any amino acid
US-10-058-993-85

Query Match 99.3%; Score 609; DB 26; Length 121;
Best Local Similarity 100.0%; Pred. No. 2e-62;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSFAGVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSFAGVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60

Qy 61 LKALSOXSTDPKESTSPKRDHDFVGMGKRVSQVQPSPTDVNOENVPSFGILKYPPRA 120
Db 61 LKALSOXSTDPKESTSPKRDHDFVGMGKRVSQVQPSPTDVNOENVPSFGILKYPPRA 120

Qy 121 E 121
Db 121 E 121

RESULT 14
US-08-879-995-1
;; Sequence 1, Application US/08879995
;; GENERAL INFORMATION:
;; APPLICANT: Hillman, Jennifer L.
;; APPLICANT: Lal, Preeti
;; APPLICANT: Kaser, Matthew R.
;; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.
;; STREET: 3174 Porter Drive
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/879,995
;; FILING DATE: Herewith
;; CLASSIFICATION: ?
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0326 US

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 122 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: BRAITUT03
;; CLONE: 2109906
US-08-879-995-1

Query Match 96.7%; Score 592.5; DB 12; Length 122;
Best Local Similarity 95.9%; Pred. No. 1.7e-60;
Matches 117; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MRIMLLFTAILAFSLAQSFAGVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSFAGVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSLEGL 60

Qy 61 LKALSOXSTDPKESTSPKRDHDFVGMGKRVSQVQPSPTDVNOENVPSFGILKYPPR 119
Db 61 LKALSOXSTDPKESTSPKRDHDFVGMGKRVSQVQPSPTDVNOENVPSFGILKYPPR 120

Qy 120 AE 121
Db 121 AE 122

RESULT 15
US-09-437-860-1
;; Sequence 1, Application US/09437860
;; GENERAL INFORMATION:
;; APPLICANT: Hillman, Jennifer L.
;; APPLICANT: Lal, Preeti
;; APPLICANT: Kaser, Matthew R.
;; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.
;; STREET: 3174 Porter Drive
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/437,860
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/879,995
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0326 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 122 amino acids
;; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT03
; CLONE: 2109906
US-09-437-860-1

Query Match 96.7%; Score 592.5; DB 18; Length 122;
Best Local Similarity 95.9%; Pred. No. 1.7e-60;
Matches 117; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
QY 1 MRIMLLFTAILAFSLAQSEFQVCKPQEVVPGGSRKRDPLQYLLQRLFKSHSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSEFQVCKPQEVVPGGSRKRDPLQYLLQRLFKSHSLEGL 60
QY 61 LKALSQXSTDPKSTSPKRDMDHDFVGMGKRSVQPDSPDTPV-NQENVPSFGILKYPPR 119
Db 61 LKALSQASTDPKSTSPKRDMDHDFVGLMGKRSVQPDSPDTPTEMXNQENVPSFGILKYPPR 120
QY 120 AE 121
Db 121 AE 122

Search completed: May 3, 2002, 12:26:39
Job time: 196 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 16:38:37 ; Search time 8.32 Seconds
(without alignments)
171.347 Million cell updates/sec

Title: US-09-852-659-85

Perfect score: 613

Sequence: 1 MRIMLLFTAILAFSLAQSGF.....DVNOENVPSGILKYPPRAE 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 59194 seqs, 11781848 residues

Total number of hits satisfying chosen parameters: 59194

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

rDatabase : Pending Patents AA_New.*

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	487	79.4	135	5	US-09-991-150-359
2	487	79.4	135	6	US-10-119-480-108
3	68	11.1	452	5	US-09-563-794B-140
4	65.5	10.7	911	1	PCT-US02-06415-6
5	65.5	10.7	911	1	PCT-US02-06415-6
6	64.5	10.5	1005	1	PCT-US02-10133-2
7	64.5	10.5	1005	5	US-09-486-861A-2
8	63	10.3	197	6	US-10-121-746-16
9	63	10.3	206	1	PCT-US02-09921-864
10	63	10.3	812	5	US-09-573-655B-347
11	63	10.3	812	5	US-09-573-655B-347
12	62	10.1	353	5	US-09-647-701A-2
13	62	10.1	452	5	US-09-563-794B-2
14	62	10.1	1394	4	US-08-945-917B-57
15	62	10.1	1449	4	US-08-945-917B-58
16	62	10.1	1528	4	US-08-945-917B-3
17	62	10.1	1583	4	US-08-945-917B-4
18	61.5	10.0	843	5	US-09-573-655B-413
19	61.5	10.0	1005	1	PCT-US02-10824-111
20	61.5	10.0	2063	1	PCT-US02-08253-204
21	61	10.0	518	5	US-09-573-655B-1620
22	61	10.0	518	5	US-09-573-655B-2273
23	60.5	9.9	828	5	US-09-540-209B-7655
24	60.5	9.9	3210	1	PCT-US02-10824-148
25	60	9.8	176	5	US-09-540-209B-8505
26	60	9.8	999	7	US-60-365-264-226

27	59.5	9.7	723	5	US-09-540-209B-5947	Sequence 5947, Ap
28	58.5	9.5	299	5	US-09-540-209B-9990	Sequence 9990, Ap
29	58.5	9.5	366	5	US-09-540-209B-6699	Sequence 6699, Ap
30	58.5	9.5	422	5	US-09-573-655B-900	Sequence 900, App
31	58.5	9.5	422	5	US-09-573-655B-1162	Sequence 1162, Ap
32	58.5	9.5	1596	5	US-09-902-432-4	Sequence 4, Appli
33	58.5	9.5	2067	1	PCT-US02-09944-778	Sequence 778, App
34	58	9.5	561	5	US-09-573-655B-2000	Sequence 2000, Ap
35	58	9.5	655	1	PCT-US02-09808-29	Sequence 29, Appl
36	57.5	9.4	86	1	PCT-US02-09921-873	Sequence 873, App
37	57.5	9.4	183	5	US-09-573-655B-1836	Sequence 1836, Ap
38	57.5	9.4	472	1	PCT-US02-09473-2	Sequence 2, Appli
39	57	9.3	124	1	PCT-US02-09820-10	Sequence 10, Appl
40	57	9.3	826	1	PCT-US02-08864-10	Sequence 10, Appl
41	57	9.3	826	1	PCT-US02-08864-6	Sequence 6, Appli
42	57	9.3	826	1	PCT-US02-08946-2	Sequence 2, Appli
43	57	9.3	826	1	PCT-US02-08946-5	Sequence 5, Appli
44	57	9.3	826	1	PCT-US02-08946-6	Sequence 6, Appli
45	57	9.3	826	1	PCT-US02-08946-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-991-150-359
; Sequence 359, Application US/09991150
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC48
; CURRENT APPLICATION NUMBER: US/09/991,150
; CURRENT FILING DATE: 2001-11-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 532
; SEQ ID NO 359
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-150-359

Query Match 79.4%; Score 487; DB 5; Length 135;
Best Local Similarity 95.0%; Pred. NO. 1.3e-48;
Matches 96; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MRIMLLFTAILAFSLAQSGFVPGGSRKRDPLDYQLLQRLFKSHSLEGL 60
DB 1 MRIMLLFTAILAFSLAQSGFVPGGSRKRDPLDYQLLQRLFKSHSLEGL 60

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Qy      61 LKALSQXSTDPKESTSPKSRDMHDFEVGXMGRSVQPDSP 101
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Db      61 LKALSQASTDPEKSTSPKSRDMHDFEVGLMGKRSVPQSGT 101

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RESULT      2
US-10-119-480-108
; Sequence 108, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 108
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-108

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RESULT      3
US-09-563-794B-140
; Sequence 140, Application US/09563794B
; GENERAL INFORMATION:
; APPLICANT: KRUGER, MARTIN
; APPLICANT: WELCH, PETER J.
; APPLICANT: BARBER, JACK R.
; TITLE OF INVENTION: CELLULAR REGULATORS OF INFECTIOUS AGENTS AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 039316-0801
; CURRENT APPLICATION NUMBER: US/09/563.794B
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 140
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-563-794B-140

Query Match      11.1%; Score 68; DB 5; Length 452;
Best Local Similarity 27.7%; Pred. No. 2.8;
Matches 23; Conservative 19; Mismatches 37; Indels 4; Gaps 3
QY 40 DPDYQLLQRLFKSHSSLEGLLKALSOXSTDPKSTSPKR--DMHDFP-VGXMGKRVSQ 96

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Db      111 DVALHEVVD-LFRAYDASLAWLRKGGESTEPVGQKGKKKTVEQRDFGVDSTGRLLF 169
          | |:::| |::: : :| |::|| |::|
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QY      97 PDSPTDVNQENVPSFGILKYPPR 119
          : |:::| |::| ||: ||
          +-----+-----+-----+-----+
Db      170 MANEADLDEELVIKGSILQKHPR 192

RESULT 4
PCT-US02-06415-6
; Sequence 6, Application PC/TUS0206415
; GENERAL INFORMATION:
; APPLICANT: St. Elizabeth's Medical Center, Inc.
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and
; FILE REFERENCE: SI237/7019WO
; CURRENT APPLICATION NUMBER: PCT/US02/06415
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-06415-6

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RESULT      5
PCT-US02-06415-8
; Sequence 8, Application PC/TUS0206415
; GENERAL INFORMATION:
; APPLICANT: St. Elizabeth's Medical Center, Inc.
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses There
; FILE REFERENCE: SI2377019WO
; CURRENT APPLICATION NUMBER: PCT/US02/06415
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-06415-8

Query Match          10.7%; Score 65.5; DB 1; Length 911;
Best Local Similarity 23.9%; Pred. No. 14;
Matches 32; Conservative 16; Mismatches 59; Indels 27; Gaps 4;

Qy      5  LLFTAILAFSLAQSGFVAVCKPQEVVPGGRSK-----RDPDLVQLLQRLFKSH 54
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Db     102  LTFWSLLELRVRFTKGTVLLDLQETSLAGVANQLIDRFIFEDQIRPDQRELLRLLIKH 161

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		matches 36, Conserva16, mismatches 16, gaps 35, indels 27,	
Db	102	LTFTWLSLELRVFTKGTIVLLDQETSLAGVANQLLDREIFEDQIRPQDRELLRALLKHH	161

;; APPLICANT: AMSHEY, Stefan R.
;; APPLICANT: DAUGHERTY, Sean C.

[illegible]


```

; APPLICANT: KRUGER, MARTIN
; APPLICANT: WELCH, PETER J.
; APPLICANT: BARBER, JACK R.
; TITLE OF INVENTION: CELLULAR REGULATORS OF INFECTIOUS AGENTS AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 039316-0801
; CURRENT APPLICATION NUMBER: US/09/563,794B
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-794B-2

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	Query Match	10.1%	Score:62;	DB 5;	Length 452;	
	Best Local Similarity	26.5%;	Pred. No. 14;	Mismatches	19;	Gaps 3;
	Matches 22;	Conservative	19;	Indels	38;	Caps 4;
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Dd	111	DVALHEVVD-LFRAYDASLAMLAKMGODSIIEPVGQGGKKKAVERQDFIGVDSTGKRLF	169			
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QY	97	PDSPDTVNQENVPISFGILKYPPR	119			
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Dd	170	MAAEADLDEELVTKGSLQKHPR	192			

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RESULT 14
US-08-945-917B-57
; Sequence 57, Application US/08945917B
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/08/945,917B
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 57
; LENGTH: 1394
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-08-945-917B-57

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Query Match	10.1%	Score 62;	DB 4;	Length 1394;
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QY	119	RA 120		
Db	356	PA 357		

RESULT 15
US-08-945-917B-58
; Sequence 58, Application US/08945917B
; GENERAL INFORMATION:

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; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/08/945, 917B
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 1449
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-08-945-917B-58

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Query Match	10.1%	Score 62;	DB 4;	Length 1449;
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Db	296	TSDEKSPSSDDLTLNASIVTAIRQPIATPVSPNIIINKPVEEKPTLAVGKVKSTAKRDP	355	
QY	119	RA 120		
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OM protein - protein search, using sw model

May 3, 2002, 12:27:23 ; Search time 106.55 Seconds
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Title: US-09-852-659-85

perfect score: 12

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SUMMARIES

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78	54.5	135	27	US-09-998-156-359	Sequence 359, App	151	7	5.8	338	27	US-09-708-427-74452	Sequence 74452, A
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83	54.5	135	27	US-09-997-333-359	Sequence 359, App	156	7	5.8	405	27	US-09-614-150-28950	Sequence 28950, A
84	54.5	135	27	US-09-997-529-359	Sequence 359, App	157	7	5.8	415	17	US-09-391-631-283	Sequence 283, App
85	54.5	135	27	US-09-997-641-359	Sequence 359, App	158	7	5.8	419	22	US-09-818-990-6	Sequence 6, Appli
86	54.5	135	27	US-09-997-857-359	Sequence 359, App	159	7	5.8	420	21	US-09-770-509-10	Sequence 10, Appli
87	54.5	135	27	US-09-990-711-359	Sequence 359, App	160	7	5.8	459	22	US-09-818-990-10	Sequence 10, Appli
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89	54.5	135	28	US-09-989-729A-359	Sequence 359, App	162	7	5.8	483	22	US-09-807-239-42	Sequence 42, Appli
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95	19.0	36	22	US-09-852-797-108	Sequence 108, App	168	7	5.8	573	24	US-60-245-225-247	Sequence 247, App
96	19.0	36	22	US-09-853-161-108	Sequence 108, App	169	7	5.8	589	24	US-60-248-505-862	Sequence 862, App
97	19.0	36	26	US-10-058-993-108	Sequence 108, App	170	7	5.8	590	5	US-08-123-932A-12	Sequence 12, Appli
98	10.8	15	15	US-09-152-060-109	Sequence 109, App	171	7	5.8	590	21	US-09-771-161A-206	Sequence 206, App
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100	10.8	15	22	US-09-852-797-109	Sequence 109, App	173	7	5.8	590	23	US-09-771-161A-208	Sequence 208, App
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103	10.8	92	14	US-09-086-078-30	Sequence 30, Appli	176	7	5.8	608	24	US-60-191-637-18659	Sequence 18659, A
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110	8.6	10	5	US-08-171-134-4	Sequence 4, Appli	183	7	5.8	913	18	US-09-488-725A-6009	Sequence 6009, Ap
111	8.6	10	6	US-08-235-401-4	Sequence 4, Appli	184	7	5.8	1145	21	US-09-758-759-167	Sequence 167, App
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115	8.6	10	7	US-08-343-750-4	Sequence 4, Appli	188	7	5.8	1316	27	US-09-708-427-18423	Sequence 18423, A
116	8.6	10	7	US-08-387-056-4	Sequence 4, Appli	189	6	5.0	9	20	US-09-657-276-545	Sequence 545, App
117	8.6	10	8	US-08-408-238-4	Sequence 4, Appli	190	6	5.0	10	3	US-07-737-371A-43	Sequence 43, Appli
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229	5.0	40	19	US-09-538-038-796	Sequence 796, App	302	6	5.0	84	16	US-09-270-849B-180965	Sequence 180965, A
230	5.0	41	24	US-60-170-346-2002	Sequence 2002, Ap	303	6	5.0	85	1	PCT-US00-05988-1083	Sequence 1083, Ap
231	5.0	41	28	US-09-455-978B-23	Sequence 23, Appl	304	6	5.0	85	1	PCT-US01-08631-34565	Sequence 34565, A
232	5.0	45	1	PCT-US01-29838-348	Sequence 348, App	305	6	5.0	85	12	US-08-827-356-2847	Sequence 2847, Ap
233	5.0	48	17	US-09-374-494-22	Sequence 22, Appl	306	6	5.0	85	19	US-09-543-681A-7741	Sequence 7741, Ap
234	5.0	48	22	US-09-851-138-22	Sequence 22, Appl	307	6	5.0	85	21	US-09-758-471-4958	Sequence 4958, Ap
235	5.0	48	24	US-60-182-093-1898	Sequence 1898, Ap	308	6	5.0	85	23	US-09-925-300-1083	Sequence 1083, Ap
236	5.0	50	1	PCT-US01-02723-305	Sequence 305, App	309	6	5.0	86	24	US-60-182-568-901	Sequence 901, App
237	5.0	50	15	US-09-146-313-49	Sequence 49, Appl	310	6	5.0	86	24	PCT-US01-01341-1286	Sequence 1286, Ap
238	5.0	50	21	US-09-707-351-305	Sequence 305, App	311	6	5.0	88	14	US-09-057-719-779	Sequence 779, App
239	5.0	50	24	US-60-182-075-59	Sequence 59, Appl	312	6	5.0	88	18	US-09-471-276-1566	Sequence 1566, Ap
240	5.0	55	20	US-09-617-682A-15153	Sequence 15153, A	313	6	5.0	88	21	US-09-764-864-1286	Sequence 1286, Ap
241	5.0	56	20	US-09-617-681A-2968	Sequence 2968, Ap	314	6	5.0	88	26	US-10-080-129-1286	Sequence 1286, Ap
242	5.0	56	24	US-60-170-430-1955	Sequence 1955, Ap	315	6	5.0	91	21	US-09-733-089-19111	Sequence 19111, A
243	5.0	56	27	US-09-675-784A-8286	Sequence 8286, Ap	316	6	5.0	91	21	US-09-816-660-19111	Sequence 19111, A
244	5.0	58	24	US-60-182-568-616	Sequence 616, App	317	6	5.0	91	22	US-60-171-461-1428	Sequence 1428, Ap
245	5.0	59	1	PCT-US01-08631-54459	Sequence 54459, A	318	6	5.0	92	13	US-08-904-468-329	Sequence 329, App
246	5.0	59	1	PCT-US01-08631-54502	Sequence 54502, A	319	6	5.0	92	24	US-60-192-587-1640	Sequence 1640, Ap
247	5.0	61	1	PCT-US01-08655-498	Sequence 498, App	320	6	5.0	92	24	US-60-192-737-1300	Sequence 1300, Ap
248	5.0	62	24	US-60-162-357-1430	Sequence 1430, Ap	321	6	5.0	92	24	US-60-194-091-1579	Sequence 1579, Ap
249	5.0	62	24	US-60-178-305-1132	Sequence 1132, Ap	322	6	5.0	92	24	US-60-194-106-796	Sequence 796, App
250	5.0	63	1	PCT-US01-29871-163	Sequence 163, App	323	6	5.0	93	1	PCT-US00-09071-123	Sequence 123, App
251	5.0	63	14	US-09-049-719-2	Sequence 2, Appl	324	6	5.0	93	16	US-09-296-622-609	Sequence 609, App
252	5.0	63	16	US-09-280-190-4	Sequence 4, Appl	325	6	5.0	93	24	US-60-195-134-1213	Sequence 1213, Ap
253	5.0	63	18	US-09-410-375-4	Sequence 4, Appl	326	6	5.0	93	28	US-09-870-759-70	Sequence 70, Appl
254	5.0	63	22	US-09-834-366-19528	Sequence 19528, A	327	6	5.0	94	24	US-60-170-346-1327	Sequence 1327, Ap
255	5.0	63	24	US-60-162-245-3023	Sequence 3023, Ap	328	6	5.0	94	24	US-60-181-996-1304	Sequence 1304, Ap
256	5.0	63	24	US-60-197-873-19528	Sequence 19528, A	329	6	5.0	94	24	US-60-182-093-1957	Sequence 1957, Ap
257	5.0	64	1	PCT-US00-14933-135	Sequence 135, App	330	6	5.0	95	24	US-60-162-247-3594	Sequence 3594, Ap
258	5.0	64	1	PCT-US01-00911-162	Sequence 162, App	331	6	5.0	95	24	US-60-169-840-7420	Sequence 7420, Ap
259	5.0	64	1	PCT-US01-00911-162	Sequence 162, App	332	6	5.0	95	24	US-60-192-587-1028	Sequence 1028, Ap
260	5.0	64	1	PCT-US01-00911-162	Sequence 162, App	333	6	5.0	95	24	US-60-194-091-1008	Sequence 1008, Ap
261	5.0	64	18	US-09-482-273-162	Sequence 162, App	334	6	5.0	96	1	PCT-US01-08656-7336	Sequence 7336, Ap
262	5.0	64	27	US-09-984-271-162	Sequence 162, App	335	6	5.0	96	17	US-09-325-932-166	Sequence 166, App
263	5.0	64	27	US-09-984-271-162	Sequence 162, App	336	6	5.0	96	17	US-09-325-932-166	Sequence 166, App
264	5.0	65	20	US-09-617-682A-4032	Sequence 4032, Ap	337	6	5.0	96	17	US-09-327-373-166	Sequence 166, App
265	5.0	65	21	US-09-758-462-1490	Sequence 1490, Ap	338	6	5.0	96	21	US-09-758-471-4924	Sequence 445, App
266	5.0	67	16	US-09-201-945-164	Sequence 164, App	339	6	5.0	96	21	US-09-758-471-4924	Sequence 4924, Ap
267	5.0	67	16	US-09-248-796-25479	Sequence 25479, A	340	6	5.0	97	1	PCT-US01-01354-17778	Sequence 17778, A
268	5.0	68	1	PCT-US01-01339-3050	Sequence 3050, Ap	341	6	5.0	97	21	US-09-764-905-17778	Sequence 17778, A
269	5.0	68	21	US-09-764-891-3050	Sequence 3050, Ap	342	6	5.0	97	22	US-09-834-366-21129	Sequence 21129, A
270	5.0	68	22	US-09-854-847-4	Sequence 4, Appl	343	6	5.0	97	22	US-09-147-499-7196	Sequence 7196, Ap
271	5.0	68	24	US-60-162-247-5063	Sequence 5063, Ap	344	6	5.0	97	24	US-60-137-873-21129	Sequence 21129, A
272	5.0	70	1	PCT-US00-07677-116	Sequence 116, App	345	6	5.0	97	24	US-10-092-399-17778	Sequence 17778, A
273	5.0	71	16	US-09-248-796-25318	Sequence 25318, A	346	6	5.0	97	26	US-09-708-427-73893	Sequence 73893, A
274	5.0	72	24	US-60-170-429-869	Sequence 869, App	347	6	5.0	98	24	US-60-177-571-4859	Sequence 4859, Ap
275	5.0	72	24	US-60-181-269-633	Sequence 633, App	348	6	5.0	98	24	US-60-182-467-2130	Sequence 2130, Ap
276	5.0	72	22	US-09-675-784A-12060	Sequence 12060, A	349	6	5.0	98	28	US-09-621-976-7310	Sequence 7310, Ap
277	5.0	74	22	US-09-834-366-23197	Sequence 23197, A	350	6	5.0	98	1	PCT-US01-08656-9054	Sequence 9054, Ap
278	5.0	74	24	US-60-147-499-6396	Sequence 6396, Ap	351	6	5.0	98	1	PCT-US97-02318-566	Sequence 566, App
279	5.0	74	24	US-60-197-873-23197	Sequence 23197, A	352	6	5.0	98	13	US-08-903-470-566	Sequence 566, App
280	5.0	74	28	US-60-621-976-6396	Sequence 6396, Ap	353	6	5.0	98	24	US-60-147-499-7310	Sequence 7310, Ap
281	5.0	75	1	PCT-US01-01354-18745	Sequence 18745, A	354	6	5.0	98	24	US-60-177-571-4859	Sequence 4859, Ap
282	5.0	75	21	US-09-758-456-347	Sequence 347, App	355	6	5.0	98	28	US-09-621-976-7310	Sequence 7310, Ap
283	5.0	75	21	US-09-764-905-18745	Sequence 18745, A	356	6	5.0	99	15	US-09-134-000-6615	Sequence 6615, Ap
284	5.0	75	24	US-60-182-568-925	Sequence 925, App	357	6	5.0	99	15	US-09-708-427-45215	Sequence 45215, A
285	5.0	76	26	US-10-092-399-17778	Sequence 17778, A	358	6	5.0	99	27	US-09-708-427-73343	Sequence 73343, A
286	5.0	76	22	US-09-854-847-12	Sequence 12, Appl	359	6	5.0	100	1	PCT-US01-08631-38558	Sequence 38558, A
287	5.0	76	24	US-60-196-712-2749	Sequence 2749, Ap	360	6	5.0	100	27	US-09-675-784A-7681	Sequence 7681, Ap
288	5.0	78	17	US-09-674-266A-317	Sequence 317, App	361	6	5.0	101	24	US-60-104-346-12	Sequence 12, Appl
289	5.0	79	17	US-09-330-781-354	Sequence 354, App	362	6	5.0	101	24	US-60-170-374-2619	Sequence 2619, Ap
290	5.0	79	22	US-09-828-769-354	Sequence 354, App	363	6	5.0	101	24	US-60-182-467-2129	Sequence 2129, Ap
291	5.0	79	24	US-60-311-261-1585	Sequence 1585, Ap	364	6	5.0	102	11	US-08-779-828-23	Sequence 23, Appl
292	5.0	79	27	US-09-708-427-81180	Sequence 81180, A	365	6	5.0	102	11	US-08-780-890-23	Sequence 23, Appl
293	5.0	80	20	US-09-617-682A-4181	Sequence 4181, Ap	366	6	5.0	102	12	US-08-864-572-23	Sequence 23, Appl
											US-09-758-442-430	Sequence 430, Appl

367	6	5.0	103	22	US-09-834-366-17345	Sequence 17345, A	440	6	5.0	129	24	US-60-169-868-5923	Sequence 5923, Ap
368	6	5.0	103	24	US-60-197-873-17345	Sequence 17345, A	441	6	5.0	129	24	US-60-178-306-1368	Sequence 1368, Ap
369	6	5.0	104	19	US-09-539-697-68	Sequence 68, Appl	442	6	5.0	130	27	US-09-708-427-46500	Sequence 46500, A
370	6	5.0	104	27	US-09-965-602-68	Sequence 68, Appl	443	6	5.0	130	27	US-09-708-427-73891	Sequence 73891, A
371	6	5.0	104	27	US-09-620-111B-7352	Sequence 7352, Ap	444	6	5.0	131	21	US-09-733-089-16723	Sequence 16723, A
372	6	5.0	105	1	PCT-US001-26524B-8420	Sequence 8420, Ap	445	6	5.0	131	22	US-09-816-660-16723	Sequence 16723, A
373	6	5.0	105	21	US-09-758-471-4440	Sequence 4440, Ap	446	6	5.0	132	24	US-60-147-189-902	Sequence 902, App
374	6	5.0	105	22	US-09-834-366-16497	Sequence 16497, A	447	6	5.0	133	16	US-09-270-767-32096	Sequence 32096, A
375	6	5.0	105	24	US-60-197-873-16497	Sequence 16497, A	448	6	5.0	133	24	US-60-169-841-1781	Sequence 1781, Ap
376	6	5.0	106	1	PCT-US001-06782-122	Sequence 122, App	449	6	5.0	134	21	US-09-735-004-4	Sequence 4, Appl1
377	6	5.0	106	20	US-09-688-052-3827	Sequence 3827, Ap	450	6	5.0	134	24	US-60-139-669-484	Sequence 484, App
378	6	5.0	106	21	US-09-758-447-762	Sequence 762, App	451	6	5.0	136	17	US-09-325-932-76	Sequence 76, Appl
379	6	5.0	107	11	US-08-728-742-9	Sequence 9, Appl1	452	6	5.0	136	17	US-09-325-932A-76	Sequence 76, Appl1
380	6	5.0	107	11	US-08-728-742A-9	Sequence 9, Appl1	453	6	5.0	136	17	US-09-327-373-76	Sequence 76, Appl1
381	6	5.0	107	16	US-09-252-691-10101	Sequence 10101, A	454	6	5.0	137	15	US-09-134-000-5195	Sequence 5195, Ap
382	6	5.0	107	16	US-09-252-691C-10101	Sequence 10101, A	455	6	5.0	137	27	US-09-977-418-36	Sequence 36, Appl
383	6	5.0	107	18	US-09-417-507-25236	Sequence 25236, A	456	6	5.0	137	28	US-09-977-033A-36	Sequence 36, Appl
384	6	5.0	109	16	US-09-270-767-47313	Sequence 47313, A	457	6	5.0	138	23	US-09-902-540A-11211	Sequence 11211, A
385	6	5.0	109	16	US-09-270-849B-182881	Sequence 182881, A	458	6	5.0	139	1	PCT-US97-04115-66	Sequence 66, Appl
386	6	5.0	110	17	US-09-325-932-77	Sequence 77, Appl	459	6	5.0	139	20	US-09-614-450-2555	Sequence 2555, Ap
387	6	5.0	110	17	US-09-325-932A-77	Sequence 77, Appl	460	6	5.0	139	27	US-09-399-118-66	Sequence 66, Appl
388	6	5.0	110	17	US-09-327-373-77	Sequence 77, Appl	461	6	5.0	140	24	US-60-186-281-316	Sequence 316, App
389	6	5.0	110	21	US-09-733-089-9219	Sequence 9219, Ap	462	6	5.0	141	1	PCT-US01-08631-42228	Sequence 42228, A
390	6	5.0	110	22	US-09-816-660-9219	Sequence 9219, Ap	463	6	5.0	141	1	PCT-US01-08631-42228	Sequence 42228, A
391	6	5.0	111	1	PCT-US01-01324-1408	Sequence 1408, Ap	464	6	5.0	141	18	US-09-417-507-27719	Sequence 27719, A
392	6	5.0	111	26	US-10-079-979-1408	Sequence 1408, Ap	465	6	5.0	141	24	US-60-178-306-1367	Sequence 1367, Ap
393	6	5.0	112	22	US-09-834-366-15953	Sequence 15953, A	466	6	5.0	141	25	US-60-361-742-612	Sequence 612, App
394	6	5.0	112	22	US-09-834-366-17543	Sequence 17543, A	467	6	5.0	142	24	US-60-196-713-3486	Sequence 3486, Ap
395	6	5.0	112	24	US-60-197-873-15953	Sequence 15953, A	468	6	5.0	143	16	US-09-252-691-8747	Sequence 8747, Ap
396	6	5.0	112	24	US-60-197-873-17543	Sequence 17543, A	469	6	5.0	143	16	US-09-252-691C-8747	Sequence 8747, Ap
397	6	5.0	113	1	PCT-US01-01338-1547	Sequence 1547, Ap	470	6	5.0	143	21	US-09-733-449-12748	Sequence 12748, A
398	6	5.0	113	1	PCT-US01-01359-98	Sequence 98, Appl	471	6	5.0	143	22	US-09-803-110-12748	Sequence 12748, A
399	6	5.0	113	21	US-09-764-863-98	Sequence 98, Appl	472	6	5.0	143	24	US-60-170-346-1550	Sequence 1550, Ap
400	6	5.0	113	21	US-09-764-877-1547	Sequence 1547, Ap	473	6	5.0	144	1	PCT-US00-05881-795	Sequence 795, App
401	6	5.0	113	24	US-60-213-178-663	Sequence 663, App	474	6	5.0	144	23	US-09-925-298-795	Sequence 795, App
402	6	5.0	113	27	US-09-989-442-98	Sequence 98, Appl	475	6	5.0	144	24	US-60-173-465-352	Sequence 352, App
403	6	5.0	113	27	US-09-708-427-73892	Sequence 73892, A	476	6	5.0	144	24	US-09-248-796-26049	Sequence 26049, A
404	6	5.0	114	1	PCT-US01-00663-36257	Sequence 36257, A	477	6	5.0	146	16	US-09-620-111B-7350	Sequence 7350, Ap
405	6	5.0	114	22	US-09-864-761-41031	Sequence 41031, A	478	6	5.0	146	27	US-09-708-427-63259	Sequence 63259, A
406	6	5.0	114	26	US-10-029-386-34154	Sequence 34154, A	479	6	5.0	148	27	US-09-708-427-63259	Sequence 63259, A
407	6	5.0	114	27	US-09-828-708-11	Sequence 11, Appl	480	6	5.0	149	24	US-60-312-544-10721	Sequence 10721, A
408	6	5.0	114	27	US-09-675-784A-13357	Sequence 13357, A	481	6	5.0	150	21	US-09-733-089-9199	Sequence 9199, Ap
409	6	5.0	115	27	US-09-675-784A-9630	Sequence 9630, Ap	482	6	5.0	150	22	US-09-816-660-9199	Sequence 9199, Ap
410	6	5.0	116	1	PCT-US97-07950-403	Sequence 403, App	483	6	5.0	150	24	US-60-171-434-1489	Sequence 1489, Ap
411	6	5.0	116	12	US-08-858-207A-403	Sequence 403, App	484	6	5.0	151	27	US-09-611-526-3409	Sequence 3409, Ap
412	6	5.0	118	15	US-09-127-238-16	Sequence 16, Appl	485	6	5.0	151	27	US-09-708-427-37421	Sequence 37421, A
413	6	5.0	118	21	US-09-758-461-677	Sequence 677, App	486	6	5.0	152	24	US-60-140-806-903	Sequence 903, App
414	6	5.0	118	21	US-09-760-469-1093	Sequence 1093, Ap	487	6	5.0	153	21	US-09-700-708-4	Sequence 4, Appl1
415	6	5.0	122	1	PCT-US01-00911-356	Sequence 256, App	488	6	5.0	153	21	US-09-758-472-5508	Sequence 5508, Ap
416	6	5.0	122	1	PCT-US01-29871-259	Sequence 259, App	489	6	5.0	153	28	US-09-455-978B-76	Sequence 76, Appl
417	6	5.0	122	1	PCT-US99-15849-251	Sequence 251, App	490	6	5.0	154	16	US-09-252-931A-24585	Sequence 24585, A
418	6	5.0	122	18	US-09-482-273-256	Sequence 256, App	491	6	5.0	154	24	US-09-732-210-859	Sequence 859, App
419	6	5.0	122	27	US-09-620-111B-7351	Sequence 7351, Ap	492	6	5.0	154	24	US-60-169-340-859	Sequence 859, App
420	6	5.0	122	27	US-09-984-276-256	Sequence 256, App	493	6	5.0	155	24	US-60-173-462-62	Sequence 62, Appl
421	6	5.0	122	27	US-09-984-271-256	Sequence 256, App	494	6	5.0	155	27	US-09-708-427-79365	Sequence 79365, A
422	6	5.0	123	20	US-09-614-450-2557	Sequence 2557, Ap	495	6	5.0	156	19	US-09-583-110-5095	Sequence 5095, Ap
423	6	5.0	123	27	US-09-708-427-79794	Sequence 79794, A	496	6	5.0	156	22	US-09-833-730-252	Sequence 252, App
424	6	5.0	124	21	US-09-758-445-610	Sequence 610, App	497	6	5.0	156	24	US-60-207-362-42	Sequence 14, Appl
425	6	5.0	124	26	US-10-015-127-13943	Sequence 13943, A	498	6	5.0	156	27	US-09-708-427-55194	Sequence 55194, A
426	6	5.0	125	1	PCT-US97-09911-34	Sequence 34, Appl	499	6	5.0	156	27	US-09-708-427-78835	Sequence 78835, A
427	6	5.0	125	1	PCT-US98-25247-317	Sequence 317, App	500	6	5.0	156	28	US-09-769-787-98	Sequence 98, Appl
428	6	5.0	125	1	PCT-US98-25247-317	Sequence 317, App	501	6	5.0	157	1	PCT-US99-05485-19	Sequence 19, Appl
429	6	5.0	125	15	US-09-199-637-317	Sequence 317, App	502	6	5.0	157	16	US-09-270-767-33788	Sequence 33788, A
430	6	5.0	125	15	US-09-199-637A-317	Sequence 317, App	503	6	5.0	157	16	US-09-270-767-49005	Sequence 49005, A
431	6	5.0	125	28	US-09-975-719-317	Sequence 317, App	504	6	5.0	157	16	US-09-270-849B-194339	Sequence 194339, A
432	6	5.0	127	1	PCT-US00-06112-715	Sequence 715, App	505	6	5.0	157	21	US-09-758-450-759	Sequence 759, App
433	6	5.0	127	20	US-09-640-211A-715	Sequence 715, App	506	6	5.0	157	24	US-60-181-328-19	Sequence 19, Appl
434	6	5.0	127	27	US-09-708-427-79793	Sequence 79793, A	507	6	5.0	157	24	PCT-US01-08631-42038	Sequence 42038, A
435	6	5.0	128	1	PCT-US01-08631-44231	Sequence 44231, A	508	6	5.0	158	1	PCT-US01-08631-42038	Sequence 42038, A
436	6	5.0	128	1	PCT-US01-08631-57130	Sequence 57130, A	509	6	5.0	158	18	US-09-417-507-23780	Sequence 23780, A
437	6	5.0	129	12	US-08-864-517-2	Sequence 2, Appl1	510	6	5.0	158	22	US-09-834-366-14169	Sequence 14169, A
438	6	5.0	129	19	US-09-502-967-36	Sequence 36, Appl	511	6	5.0	158	24	US-60-197-873-14169	Sequence 14169, A
439	6	5.0	129	24	US-60-160-209-4028	Sequence 4028, Ap	512	6	5.0	159	28	US-09-628-987B-993	Sequence 993, App

659	6	5.0	229	16	US-09-270-767-44085	Sequence 44085, A	732	6	5.0	244	27	US-09-897-516-6687	Sequence 6687, Ap
660	6	5.0	229	18	US-09-428-944-871	Sequence 871, App	733	6	5.0	245	1	PCT-US99-09034-38	Sequence 38, Appl
661	6	5.0	229	27	US-09-675-784A-8532	Sequence 8532, Ap	734	6	5.0	245	18	US-09-488-725A-6814	Sequence 6814, Ap
662	6	5.0	231	12	US-08-808-031-32	Sequence 32, Appl	735	6	5.0	246	24	US-60-248-798-206	Sequence 206, App
663	6	5.0	231	12	US-08-808-031A-34	Sequence 34, Appl	736	6	5.0	246	27	US-09-708-427-5592	Sequence 5592, A
664	6	5.0	232	1	PCT-US01-08631-57050	Sequence 57050, A	737	6	5.0	247	1	PCT-US00-28664A-57	Sequence 57, Appl
665	6	5.0	233	16	US-09-252-991A-23516	Sequence 23516, A	738	6	5.0	247	19	US-09-573-655A-977	Sequence 977, App
666	6	5.0	233	23	US-09-948-941-491	Sequence 491, App	739	6	5.0	247	22	US-09-832-129-57	Sequence 57, Appl
667	6	5.0	233	27	US-09-675-784A-10554	Sequence 10554, A	740	6	5.0	248	18	US-09-417-507-38933	Sequence 38933, A
668	6	5.0	234	23	US-09-902-540-12262	Sequence 10554, A	741	6	5.0	249	16	US-09-248-796-26797	Sequence 26797, A
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671	6	5.0	235	14	US-09-001-403-27	Sequence 27, Appl	744	6	5.0	250	27	US-09-594-595B-754	Sequence 754, App
672	6	5.0	235	14	US-09-046-316-2	Sequence 2, Appl	745	6	5.0	251	27	US-09-594-595B-754	Sequence 754, App
673	6	5.0	235	15	US-09-167-513-2	Sequence 2, Appl	746	6	5.0	252	16	US-09-252-691C-11180	Sequence 11180, A
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676	6	5.0	235	18	US-09-467-870-2	Sequence 99, Appl	749	6	5.0	253	16	US-09-248-796-27637	Sequence 27637, A
677	6	5.0	235	18	US-09-469-099-14	Sequence 2, Appl	750	6	5.0	253	27	US-09-605-703B-1138	Sequence 1138, Ap
678	6	5.0	235	21	US-09-702-114A-2	Sequence 14, Appl	751	6	5.0	255	16	US-09-248-796-18600	Sequence 18600, A
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683	6	5.0	235	23	US-09-943-851-91	Sequence 91, Appl	756	6	5.0	259	17	US-09-393-022-127	Sequence 127, App
684	6	5.0	235	23	US-09-944-403-91	Sequence 91, Appl	757	6	5.0	259	27	US-09-798-889-127	Sequence 127, App
685	6	5.0	235	23	US-09-944-413-91	Sequence 91, Appl	758	6	5.0	260	19	US-09-543-681A-8210	Sequence 8210, Ap
686	6	5.0	235	23	US-09-944-449-91	Sequence 91, Appl	759	6	5.0	260	24	US-60-245-225-319	Sequence 319, App
687	6	5.0	235	23	US-09-944-457-91	Sequence 91, Appl	760	6	5.0	260	24	US-60-258-250-95	Sequence 95, Appl
688	6	5.0	235	23	US-09-944-654-91	Sequence 91, Appl	761	6	5.0	260	27	US-09-708-427-70385	Sequence 70385, A
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690	6	5.0	235	23	US-09-944-944-91	Sequence 91, Appl	763	6	5.0	261	14	US-09-050-739-145	Sequence 145, App
691	6	5.0	235	23	US-09-945-015-91	Sequence 91, Appl	764	6	5.0	261	14	US-09-246-191-145	Sequence 145, App
692	6	5.0	235	23	US-09-945-584-91	Sequence 91, Appl	765	6	5.0	261	21	US-09-791-171-145	Sequence 145, App
693	6	5.0	235	23	US-09-945-587-91	Sequence 91, Appl	766	6	5.0	261	27	US-09-943-443-145	Sequence 145, App
694	6	5.0	235	26	US-10-002-796-32	Sequence 91, Appl	767	6	5.0	261	28	US-09-804-980-145	Sequence 145, App
695	6	5.0	235	26	US-10-028-072-390	Sequence 32, Appl	768	6	5.0	262	1	PCT-US98-12076-31	Sequence 31, Appl
696	6	5.0	235	26	US-10-066-193-32	Sequence 390, App	769	6	5.0	262	14	US-09-096-287-31	Sequence 31, Appl
697	6	5.0	235	26	US-10-066-198-32	Sequence 32, Appl	770	6	5.0	262	18	US-09-417-507-28482	Sequence 28482, A
698	6	5.0	235	26	US-10-066-211-32	Sequence 32, Appl	771	6	5.0	262	18	US-09-488-725A-2018	Sequence 2018, Ap
699	6	5.0	235	26	US-10-066-269-32	Sequence 32, Appl	772	6	5.0	262	21	PCT-US98-746-783-65	Sequence 65, Appl
700	6	5.0	235	26	US-10-066-273-32	Sequence 32, Appl	773	6	5.0	265	1	PCT-US98-25247-57	Sequence 57, Appl
701	6	5.0	235	26	US-10-066-500-32	Sequence 32, Appl	774	6	5.0	265	15	PCT-US98-25247-57	Sequence 57, Appl
702	6	5.0	235	26	US-10-081-036-68	Sequence 32, Appl	775	6	5.0	265	15	US-09-199-637-57	Sequence 57, Appl
703	6	5.0	235	26	US-10-066-203-32	Sequence 68, Appl	776	6	5.0	265	15	US-09-199-637A-57	Sequence 57, Appl
704	6	5.0	235	26	US-10-066-494-32	Sequence 32, Appl	777	6	5.0	265	20	US-09-644-095-2	Sequence 2, Appl
705	6	5.0	235	27	US-09-944-097-91	Sequence 91, Appl	778	6	5.0	265	20	US-09-644-095-4	Sequence 4, Appl
706	6	5.0	235	27	US-09-944-896-91	Sequence 91, Appl	779	6	5.0	265	26	US-10-072-851-12297	Sequence 12297, A
707	6	5.0	235	27	US-09-943-851A-91	Sequence 91, Appl	780	6	5.0	265	26	US-10-072-851-12873	Sequence 12873, A
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709	6	5.0	235	27	US-09-944-929-91	Sequence 91, Appl	782	6	5.0	265	28	US-09-815-242-12873	Sequence 12873, A
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712	6	5.0	235	27	US-09-599-360B-14	Sequence 14, Appl	785	6	5.0	266	19	US-09-583-110-3761	Sequence 3761, Ap
713	6	5.0	235	27	US-09-944-396-91	Sequence 91, Appl	786	6	5.0	266	19	US-09-675-784A-12878	Sequence 12878, A
714	6	5.0	235	27	US-09-944-432-91	Sequence 91, Appl	787	6	5.0	267	16	US-09-252-631-8178	Sequence 8178, Ap
715	6	5.0	236	15	US-09-134-000-4896	Sequence 91, Appl	788	6	5.0	267	16	US-09-252-691C-8178	Sequence 8178, Ap
716	6	5.0	236	15	US-09-902-540-16750	Sequence 16750, A	789	6	5.0	268	18	US-09-417-507-41802	Sequence 41802, A
717	6	5.0	237	16	US-09-270-767-39303	Sequence 39303, A	790	6	5.0	268	26	US-10-029-386-33381	Sequence 33381, A
718	6	5.0	237	16	US-09-270-767-54520	Sequence 54520, A	791	6	5.0	268	25	US-60-339-453-348	Sequence 348, App
719	6	5.0	237	16	US-09-270-849B-190954	Sequence 190954, A	792	6	5.0	272	27	US-09-708-427-55051	Sequence 55051, A
720	6	5.0	238	21	US-09-758-442-536	Sequence 536, App	793	6	5.0	272	27	US-09-708-427-79742	Sequence 79742, A
721	6	5.0	239	21	US-09-758-465-706	Sequence 706, App	794	6	5.0	273	1	PCT-US00-29360-227	Sequence 227, App
722	6	5.0	239	27	US-09-801-368-300	Sequence 300, App	795	6	5.0	273	27	US-09-708-427-69911	Sequence 69911, A
723	6	5.0	239	27	US-09-487-558-300	Sequence 300, App	796	6	5.0	274	18	US-09-488-725A-5590	Sequence 5590, Ap
724	6	5.0	239	27	US-09-708-427-2976	Sequence 2976, Ap	797	6	5.0	275	16	US-09-270-767-57659	Sequence 57659, A
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727	6	5.0	240	17	US-09-387-372-3	Sequence 2, Appl	800	6	5.0	276	17	US-09-352-994A-7	Sequence 7, Appl
728	6	5.0	241	17	US-09-248-796-14587	Sequence 14587, A	801	6	5.0	276	17	US-09-352-994A-7	Sequence 7, Appl
729	6	5.0	242	15	US-09-167-513-18	Sequence 18, Appl	802	6	5.0	277	12	US-09-134-001C-5612	Sequence 5612, Ap
730	6	5.0	243	15	US-09-167-513-18	Sequence 18, Appl	803	6	5.0	277	15	US-09-450-969-7379	Sequence 7379, Ap
731	6	5.0	244	24	US-60-215-161-6687	Sequence 6687, Ap	804	6	5.0	277	18		

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807	6	5.0	278	21	US-09-738-626-4303	Sequence 4303, Ap	880	6	5.0	316	16	US-09-248-796-19060	Sequence 19060, A
808	6	5.0	278	24	US-60-324-631-1068	Sequence 1068, Ap	881	6	5.0	319	24	US-60-173-464-18854	Sequence 18854, A
809	6	5.0	279	1	PCT-US01-08631-47976	Sequence 47976, A	882	6	5.0	319	24	US-60-191-637-22979	Sequence 22979, A
810	6	5.0	279	21	US-09-757-026-392	Sequence 392, App	883	6	5.0	319	24	US-60-191-681-18125	Sequence 18125, A
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812	6	5.0	281	1	PCT-US01-08631-47074	Sequence 47074, A	885	6	5.0	320	1	PCT-US97-01072-61	Sequence 61, Appl
813	6	5.0	281	12	US-08-827-356-2810	Sequence 2810, Ap	886	6	5.0	320	1	PCT-US97-21783-102	Sequence 102, Appl
814	6	5.0	281	20	US-09-611-529-5278	Sequence 5278, Ap	887	6	5.0	320	17	US-09-308-825A-102	Sequence 102, App
815	6	5.0	281	21	US-09-758-471-4470	Sequence 4470, Ap	888	6	5.0	320	27	US-09-684-938-102	Sequence 61, Appl
816	6	5.0	282	16	US-09-248-796-17101	Sequence 4770, Ap	888	6	5.0	320	28	US-09-350-597-61	Sequence 61, Appl
817	6	5.0	283	1	PCT-US01-08631-37177	Sequence 37177, A	889	6	5.0	320	28	US-09-350-597-61	Sequence 61, Appl
818	6	5.0	283	16	US-09-252-991A-24178	Sequence 24178, A	890	6	5.0	320	28	US-09-350-597-61	Sequence 61, Appl
819	6	5.0	283	24	US-60-167-217-512	Sequence 512, App	891	6	5.0	321	24	US-60-312-544-10720	Sequence 10720, A
820	6	5.0	284	1	US-60-245-227-51	Sequence 51, Appl	893	6	5.0	322	8	US-08-402-601A-89	Sequence 89, Appl
821	6	5.0	284	1	PCT-US01-08631-56920	Sequence 56920, A	894	6	5.0	322	9	US-08-520-946-89	Sequence 89, Appl
822	6	5.0	284	18	US-09-434-968-78	Sequence 78, Appl	895	6	5.0	322	12	US-08-802-233-89	Sequence 89, Appl
823	6	5.0	285	15	US-09-107-433-4223	Sequence 4223, Ap	896	6	5.0	322	18	US-09-417-507-43060	Sequence 43060, A
824	6	5.0	286	1	PCT-US01-08631-32802	Sequence 32802, A	897	6	5.0	323	1	PCT-US01-01239-1382	Sequence 1382, A
825	6	5.0	286	20	US-09-674-741-12	Sequence 12, Appl	898	6	5.0	323	21	US-09-764-902-1382	Sequence 1382, Ap
826	6	5.0	286	27	US-09-675-784A-10608	Sequence 10608, A	898	6	5.0	325	18	US-09-468-253A-16	Sequence 16, Appl
827	6	5.0	287	24	US-60-146-315-626	Sequence 626, App	900	6	5.0	325	21	US-09-738-626-6072	Sequence 6072, Ap
828	6	5.0	288	21	US-09-738-626-5463	Sequence 5463, Ap	901	6	5.0	325	21	US-09-760-476-1769	Sequence 1769, Ap
829	6	5.0	288	27	US-09-708-427-54802	Sequence 54802, A	902	6	5.0	327	1	PCT-US01-29871-149	Sequence 149, App
830	6	5.0	290	24	US-60-312-544-7885	Sequence 7885, Ap	903	6	5.0	327	32	PCT-US02-08123-1199	Sequence 1199, App
831	6	5.0	291	21	US-09-758-460-4788	Sequence 498, App	904	6	5.0	327	32	PCT-US02-08124-501	Sequence 501, App
832	6	5.0	294	20	US-09-674-741-17	Sequence 17, Appl	905	6	5.0	327	32	PCT-US02-08276-374	Sequence 374, App
833	6	5.0	294	21	US-09-758-441-304	Sequence 304, App	906	6	5.0	327	32	PCT-US02-08277-790	Sequence 790, App
834	6	5.0	295	1	PCT-US01-14827-9723	Sequence 9723, Ap	907	6	5.0	328	1	PCT-US01-00911-148	Sequence 148, App
835	6	5.0	296	1	PCT-US00-05988-1231	Sequence 1231, Ap	908	6	5.0	328	1	PCT-US99-15849-148	Sequence 148, App
836	6	5.0	296	23	US-09-925-300-1231	Sequence 1231, Ap	909	6	5.0	328	18	US-09-482-273-148	Sequence 148, App
837	6	5.0	297	21	US-09-708-427-27166	Sequence 27166, A	910	6	5.0	328	18	US-09-482-273-148	Sequence 148, App
838	6	5.0	297	21	US-09-738-626-6303	Sequence 6303, Ap	911	6	5.0	328	19	US-09-513-597-2	Sequence 2, Appli
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840	6	5.0	299	12	US-08-827-356-4535	Sequence 4535, Ap	913	6	5.0	328	27	US-09-984-271-148	Sequence 148, App
841	6	5.0	299	20	US-09-611-529-7221	Sequence 7221, Ap	913	6	5.0	329	24	US-60-245-241-147	Sequence 147, App
842	6	5.0	300	17	US-09-328-352-4146	Sequence 4146, Ap	914	6	5.0	329	24	US-60-258-016-39	Sequence 39, Appl
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844	6	5.0	300	19	US-09-585-858-42	Sequence 42, Appl	916	6	5.0	331	1	PCT-US01-08631-41692	Sequence 41692, A
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846	6	5.0	300	22	US-09-816-660-8995	Sequence 8995, Ap	918	6	5.0	331	27	US-09-708-427-55049	Sequence 55049, A
847	6	5.0	301	27	US-09-675-784A-7239	Sequence 7239, Ap	919	6	5.0	332	1	PCT-US01-08631-32979	Sequence 32979, A
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849	6	5.0	303	20	US-09-692-059-13	Sequence 13, Appl	921	6	5.0	332	21	US-09-738-626-5809	Sequence 5809, Ap
850	6	5.0	303	24	US-60-145-988-159	Sequence 159, Appl	922	6	5.0	332	21	US-09-792-024-73	Sequence 73, Appl
851	6	5.0	305	1	PCT-US01-08631-43514	Sequence 43514, A	923	6	5.0	332	24	US-60-259-128-4703	Sequence 4703, Ap
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853	6	5.0	305	21	US-09-739-449-10966	Sequence 10966, A	925	6	5.0	332	26	US-10-032-585-7021	Sequence 7021, Ap
854	6	5.0	305	22	US-09-803-110-10966	Sequence 10966, A	926	6	5.0	332	26	US-10-072-851-14965	Sequence 14965, A
855	6	5.0	305	27	US-09-708-427-55050	Sequence 55050, A	927	6	5.0	332	32	PCT-US02-03987-14965	Sequence 14965, A
856	6	5.0	305	27	US-09-708-427-79741	Sequence 79741, A	928	6	5.0	333	18	US-09-488-725A-7007	Sequence 7007, Ap
857	6	5.0	306	1	PCT-US01-08631-39244	Sequence 39244, A	929	6	5.0	333	21	US-09-771-161-147	Sequence 147, App
858	6	5.0	306	27	US-09-708-427-54801	Sequence 54801, A	930	6	5.0	333	21	US-09-771-161A-147	Sequence 147, App
859	6	5.0	310	8	US-08-402-601A-88	Sequence 34801, A	931	6	5.0	334	24	US-60-312-544-8280	Sequence 8280, App
860	6	5.0	310	9	US-08-520-946-88	Sequence 88, Appl	932	6	5.0	335	1	PCT-US01-08631-55216	Sequence 55216, A
861	6	5.0	310	12	US-08-802-233-88	Sequence 88, Appl	933	6	5.0	335	19	US-09-538-092-811	Sequence 811, App
862	6	5.0	310	16	US-09-270-767-42373	Sequence 42373, A	934	6	5.0	335	27	US-09-182-616-4	Sequence 4, Appli
863	6	5.0	311	24	US-60-167-217-15862	Sequence 15862, A	935	6	5.0	335	27	US-09-378-261-4	Sequence 4, Appli
864	6	5.0	311	24	US-60-191-637-15866	Sequence 15866, A	936	6	5.0	336	21	US-09-760-476-1666	Sequence 1666, App
865	6	5.0	311	27	US-09-708-427-65444	Sequence 65444, A	937	6	5.0	336	21	US-09-760-479-689	Sequence 689, App
866	6	5.0	311	27	US-09-614-150-15822	Sequence 15822, A	938	6	5.0	336	21	US-09-708-427-2602	Sequence 895, App
867	6	5.0	312	17	US-09-486-334-4	Sequence 4, Appli	939	6	5.0	337	27	US-09-675-784A-12132	Sequence 2602, Ap
868	6	5.0	312	20	US-09-674-741-18	Sequence 18, Appl	940	6	5.0	337	27	PCT-US00-15410A-9	Sequence 12132, A
869	6	5.0	313	1	PCT-US01-08631-41524	Sequence 41524, A	941	6	5.0	337	1	PCT-US00-15410A-44	Sequence 9, Appli
870	6	5.0	313	16	US-09-252-691-10495	Sequence 10495, A	942	6	5.0	337	1	PCT-US01-08117-20	Sequence 44, Appl
871	6	5.0	313	16	US-09-252-691C-10495	Sequence 10495, A	943	6	5.0	337	24	PCT-US01-08117-20	Sequence 20, Appl
872	6	5.0	313	24	US-60-142-896-1068	Sequence 1068, Ap	944	6	5.0	337	27	US-60-188-986-20	Sequence 20, Appl
873	6	5.0	314	16	US-09-252-991A-27537	Sequence 27537, A	945	6	5.0	337	27	US-09-585-645-9	Sequence 9, Appli
874	6	5.0	314	24	US-60-135-519-14	Sequence 14, Appl	946	6	5.0	337	28	US-09-585-645-44	Sequence 44, Appl
875	6	5.0	314	27	US-09-708-427-65443	Sequence 65443, A	947	6	5.0	337	28	US-09-980-381-9	Sequence 9, Appli
876	6	5.0	315	8	US-08-402-601A-91	Sequence 91, Appl	948	6	5.0	338	21	US-09-980-381-44	Sequence 44, Appl
877	6	5.0	315	9	US-08-520-946-91	Sequence 91, Appl	949	6	5.0	338	21	US-09-758-463-1090	Sequence 1090, Ap
	6	5.0	315	9	US-08-520-946-91	Sequence 91, Appl	950	6	5.0	339	26	US-10-072-851-13545	Sequence 13545, A
	6	5.0	315	9	US-08-520-946-91	Sequence 91, Appl						US-09-815-242-13545	Sequence 13545, A

951 6 339 32 PCT-US02-03987-13545
952 6 340 16 US-09-270-767-40453
953 6 340 16 US-09-270-767-55669
954 6 340 16 US-09-270-849B-193369
955 6 341 18 US-09-468-253A-14
956 6 342 1 PCT-US98-20775-123
957 6 342 5 US-08-100-486-3
958 6 342 16 US-09-281-976-125
959 6 342 17 US-09-489-039A-7552
960 6 343 27 US-09-708-427-54800
961 6 344 24 US-60-173-464-29245
962 6 345 24 US-60-173-464-441
963 6 345 24 US-60-191-637-534
964 6 345 24 US-60-191-637-38368
965 6 345 24 US-60-191-681-423
966 6 345 24 US-60-191-681-29752
967 6 345 27 US-09-708-427-6029
968 6 345 27 US-09-614-150-534
969 6 345 27 US-09-614-150-38742
970 6 346 27 US-09-708-427-6028
971 6 348 1 PCT-US99-11576-10
972 6 348 8 US-08-462-966-2
973 6 348 17 US-09-318-271-10
974 6 348 20 US-09-624-183-2
975 6 348 24 US-60-125-084-10
976 6 350 16 US-09-252-691-7362
977 6 350 16 US-09-252-691C-7362
978 6 350 21 US-09-760-469-1086
979 6 350 24 US-60-215-161-6420
980 6 350 27 US-09-897-516-6420
981 6 350 27 US-09-281-646A-9
982 6 350 27 US-09-708-427-65442
983 6 356 21 US-09-738-626-6651
984 6 356 27 US-09-708-427-7472
985 6 358 21 US-09-733-089-23892
986 6 358 22 US-09-816-660-23892
987 6 359 1 PCT-US94-08055-4
988 6 359 18 US-09-417-507-43054
989 6 359 19 US-09-595-335A-297
990 6 359 26 US-10-044-643-51
991 6 359 26 US-10-044-643-52
992 6 359 27 US-09-708-427-10316
993 6 359 28 US-09-966-871-81
994 6 360 13 US-08-993-002A-6956
995 6 360 26 US-10-072-851-11378
996 6 360 27 US-09-815-242-11378
997 6 360 32 PCT-US02-03987-11378
998 6 361 1 PCT-US01-08631-50939
999 6 361 21 US-09-733-089-21818
1000 6 361 22 US-09-816-660-21818

ALIGNMENTS

RESULT 1

US-09-152-060-85

; Sequence 85, Application US/09152060

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 28 Human Secreted Proteins

; FILE REFERENCE: P2003P4

; CURRENT APPLICATION NUMBER: US/09/152,060

; CURRENT FILING DATE: 1998-09-11

; EARLIER APPLICATION NUMBER: PCT/US98/04858

; EARLIER FILING DATE: 1998-03-12

; EARLIER APPLICATION NUMBER: 60/040,762

; EARLIER FILING DATE: 1997-03-14

; EARLIER APPLICATION NUMBER: 60/040,710

; EARLIER FILING DATE: 1997-03-14

; EARLIER APPLICATION NUMBER: 60/050,934

; EARLIER FILING DATE: 1997-05-30

; EARLIER APPLICATION NUMBER: 60/048,100

; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (67)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (89)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-152-060-85

Query Match 98.3%; Score 119; DB 15; Length 121;

Best Local Similarity 100.0%; Pred.No. 6.2e-112; Indels 0; Gaps 0;
Matches 121; Conservative 0; Mismatches 0;

QY 1 MRIMLFTAILAFSLAQSGAVCKEPQEEVPGGSRKRDPPDLYQLLQRLFKSHSLEGL 60

|||||

Db 1 MRIMLFTAILAFSLAQSGAVCKEPQEEVPGGSRKRDPPDLYQLLQRLFKSHSLEGL 60

QY 61 LKALSOXSTDPEKRDMDHDFVGMGRSVQDPDPTDQNVNPSFGILKYPRA 120

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Db 61 LKALSOXSTDPEKRDMDHDFVGMGRSVQDPDPTDQNVNPSFGILKYPRA 120

QY 121 E 121

Db 121 E 121

RESULT 2

US-09-852-659-85

; Sequence 85, Application US/09852659

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 28 Human Secreted Proteins

; FILE REFERENCE: P2003P4

; CURRENT APPLICATION NUMBER: US/09/852,659

; CURRENT FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: 60/265,583

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/152,060

; PRIOR FILING DATE: 1998-09-11

; PRIOR APPLICATION NUMBER: PCT/US98/04858

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/040,762

; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/040,710

; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/050,934

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,100

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,357

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,189

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/057,765

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; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (89)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-659-85

Query Match          98.3%; Score 119; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.2e-112;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSGFAGVCKEPQEEVPGGGRSRKRDPLDYLQLLQRLFKSHSLEGL 60
    |||||||
Db 1 MRIMLLFTAILAFSLAQSGFAGVCKEPQEEVPGGGRSRKRDPLDYLQLLQRLFKSHSLEGL 60
    |||||||
Qy 61 LKALSOXSTDPKESTSPKRDHDFVCGMGKRSVQPSPTDVNQENVPFSGILKYPRA 120
    |||||||
Db 61 LKALSOXSTDPKESTSPKRDHDFVCGMGKRSVQPSPTDVNQENVPFSGILKYPRA 120
    |||||||
Qy 121 E 121
Db 121 E 121

RESULT 4
US-09-853-161-85
; Sequence 85, Application US/09853161
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (67)

; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (89)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-659-85

Query Match          98.3%; Score 119; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.2e-112;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSGFAGVCKEPQEEVPGGGRSRKRDPLDYLQLLQRLFKSHSLEGL 60
    |||||||
Db 1 MRIMLLFTAILAFSLAQSGFAGVCKEPQEEVPGGGRSRKRDPLDYLQLLQRLFKSHSLEGL 60
    |||||||
Qy 61 LKALSOXSTDPKESTSPKRDHDFVCGMGKRSVQPSPTDVNQENVPFSGILKYPRA 120
    |||||||
Db 61 LKALSOXSTDPKESTSPKRDHDFVCGMGKRSVQPSPTDVNQENVPFSGILKYPRA 120
    |||||||
Qy 121 E 121
Db 121 E 121

RESULT 3
US-09-852-797-85
; Sequence 85, Application US/09852797
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
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; FILE REFERENCE: 81.US1.PRO
; CURRENT APPLICATION NUMBER: US/60/197.873
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 13657
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -18..-1
US-60-197-873-13657

Query Match          54.5%; Score 66; DB 24; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8e-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSFQAVCKEPOEVEVPGGSRKRDPLDYQLLQRLFKSHSLEGL 60
    |||
Db 1 MRIMLLFTAILAFSLAQSFQAVCKEPOEVEVPGGSRKRDPLDYQLLQRLFKSHSLEGL 60
    |||

Qy 61 LKALSQ 66
    |||
Db 61 LKALSQ 66

RESULT 8
US-09-086-078-2
; Sequence 2, Application US/09086078
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NEUROKININ B PRECURSORS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics
; STREET: 1201 Eastlake Ave. E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,078
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan E
; REGISTRATION NUMBER: 41,156
; REFERENCE/DOCKET NUMBER: 97-26
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-086-078-2
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Query Match          54.5%; Score 66; DB 14; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.1e-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSFQAVCKEPOEVEVPGGSRKRDPLDYQLLQRLFKSHSLEGL 60
    |||
Db 1 MRIMLLFTAILAFSLAQSFQAVCKEPOEVEVPGGSRKRDPLDYQLLQRLFKSHSLEGL 60
    |||

Qy 61 LKALSQ 66
    |||
Db 61 LKALSQ 66

RESULT 9
US-09-111-901-2
; Sequence 2, Application US/09111901
; GENERAL INFORMATION:
; APPLICANT: DUCKWORTH, DAVID
; APPLICANT: HASTINGS, GREGG
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,901
; FILING DATE: 08-JULY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 97305215.2
; FILING DATE: 14-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30331
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-111-901-2

Query Match          54.5%; Score 66; DB 15; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.1e-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSFQAVCKEPOEVEVPGGSRKRDPLDYQLLQRLFKSHSLEGL 60
    |||
Db 1 MRIMLLFTAILAFSLAQSFQAVCKEPOEVEVPGGSRKRDPLDYQLLQRLFKSHSLEGL 60
    |||

Qy 61 LKALSQ 66
    |||
Db 61 LKALSQ 66

RESULT 10
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```
US-09-152-060-68
; Sequence 68, Application US/09152060
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-68
```

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Query Match      54.5%; Score 66; DB 15; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.le-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPQEEVYPGGGSKRDPDLYQLQLRFLKSHSLEGL 60
   |||||||
Db 1 MRIMLLFTAILAFSLAQSGAVCKEPQEEVYPGGGSKRDPDLYQLQLRFLKSHSLEGL 60

QY 61 LKALSQ 66
   |||||
Db 61 LKALSQ 66

RESULT 11
US-09-852-659-68
; Sequence 68, Application US/09852659
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
```

```
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659-68
```

```
Query Match      54.5%; Score 66; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.le-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPQEEVYPGGGSKRDPDLYQLQLRFLKSHSLEGL 60
   |||||||
Db 1 MRIMLLFTAILAFSLAQSGAVCKEPQEEVYPGGGSKRDPDLYQLQLRFLKSHSLEGL 60

QY 61 LKALSQ 66
   |||||
Db 61 LKALSQ 66
```

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RESULT 12
US-09-852-797-68
; Sequence 68, Application US/09852797
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-68
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Query Match 54.5%; Score 66; DB 22; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.1e-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13

US-09-853-161-68
; Sequence 68, Application US/09853161
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/048,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-68

Query Match 54.5%; Score 66; DB 22; Length 121;
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Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 LKALSQ 66
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Db 61 LKALSQ 66

RESULT 14

US-10-058-993-68
; Sequence 68, Application US/10058993
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-68

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QY 61 LKALSQ 66
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Db 61 LKALSQ 66

RESULT 15

US-08-879-995-1
; Sequence 1, Application US/08879995
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/879,995
FILING DATE: Herewith
CLASSIFICATION: ?
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0326 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-853-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT03
CLONE: 2109906
US-08-879-995-1

Query Match 54.5%; Score 66; DB 12; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.1e-58;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 LKALSQ 66
Db 61 LKALSQ 66

Search completed: May 3, 2002, 12:31:13
Job time: 230 sec

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OM protein - protein search, using sw model

Run on: May 3, 2002, 16:38:52 ; Search time 8.51 Seconds
(without alignments)
167.521 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 121
Sequence: 1 MRTLLEFLLAFSLAQSGF.....DVNQENVPSGILKYPRAE 121

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Searched: 59194 seqs, 11781848 residues

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Total number of hits satisfying chosen parameters: 59194

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	6	5.0	63	6	US-10-103-295-163
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9	6	5.0	105	6	US-10-106-698-8430
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116	5	4.1	47	1	PCr-US02-09105-240	Sequence 240, App	189	5	4.1	150	6	US-10-006-117A-196	Sequence 196, App
117	5	4.1	47	1	PCr-US02-09257-320	Sequence 320, App	190	5	4.1	150	6	US-10-006-172A-196	Sequence 196, App
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119	5	4.1	47	1	PCr-US02-09257-3193	Sequence 3193, Ap	192	5	4.1	150	6	US-10-006-768A-196	Sequence 196, App
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151	5	4.1	95	5	US-09-540-209B-8687	Sequence 8687, Ap	224	5	4.1	155	6	US-10-121-045-380	Sequence 380, App
152	5	4.1	102	5	US-09-540-209B-8744	Sequence 8744, Ap	225	5	4.1	155	6	US-10-121-046-380	Sequence 380, App
153	5	4.1	102	6	US-10-106-698-4988	Sequence 4898, Ap	226	5	4.1	155	6	US-10-121-051-380	Sequence 380, App
154	5	4.1	103	5	US-09-573-655B-1457	Sequence 1457, Ap	227	5	4.1	157	7	US-60-365-384-625	Sequence 625, App
155	5	4.1	106	7	US-60-365-384-608	Sequence 608, App	228	5	4.1	159	6	US-10-106-698-4748	Sequence 4748, Ap
156	5	4.1	107	6	US-10-116-355-344	Sequence 344, App	229	5	4.1	162	5	US-09-573-655B-2460	Sequence 2460, Ap
157	5	4.1	109	1	PCr-US02-09921-1143	Sequence 1143, Ap	230	5	4.1	162	5	US-09-540-209B-7657	Sequence 7657, Ap
158	5	4.1	115	5	US-09-540-209B-5268	Sequence 5268, Ap	231	5	4.1	163	6	US-10-017-066-7	Sequence 7, Appl
159	5	4.1	115	5	US-09-990-004A-74	Sequence 74, Appl	232	5	4.1	164	5	US-09-312-283B-385	Sequence 385, App
160	5	4.1	115	6	US-10-060-255-76	Sequence 76, Appl	233	5	4.1	164	6	US-10-103-196-21	Sequence 21, Appl
161	5	4.1	119	5	US-09-990-004A-70	Sequence 70, Appl	234	5	4.1	165	1	PCr-US02-10824-115	Sequence 115, App
162	5	4.1	121	6	US-10-006-063A-354	Sequence 354, App	235	5	4.1	169	1	PCr-US02-09785-862	Sequence 862, App
163	5	4.1	121	6	US-10-006-117A-354	Sequence 354, App	236	5	4.1	172	5	US-09-540-209B-7055	Sequence 7055, Ap
164	5	4.1	121	6	US-10-006-130A-354	Sequence 354, App	237	5	4.1	172	6	US-10-115-192-6	Sequence 6, Appl
165	5	4.1	121	6	US-10-006-172A-354	Sequence 354, App	238	5	4.1	176	6	US-10-102-806-657	Sequence 657, App
166	5	4.1	121	6	US-10-006-768A-354	Sequence 354, App	239	5	4.1	176	6	US-10-102-806-657	Sequence 218, App
167	5	4.1	121	6	US-10-106-698-6760	Sequence 6760, Ap	240	5	4.1	176	6	US-10-121-049-98	Sequence 98, Appl
168	5	4.1	121	6	US-10-017-527A-354	Sequence 354, App	241	5	4.1	176	6	US-10-121-050-98	Sequence 98, Appl
169	5	4.1	121	6	US-10-017-527A-354	Sequence 354, App	242	5	4.1	176	6	US-10-121-053-98	Sequence 98, Appl
170	5	4.1	121	6	US-10-006-041A-354	Sequence 354, App	243	5	4.1	176	6	US-10-121-043-98	Sequence 98, Appl
171	5	4.1	121	6	US-10-006-818A-354	Sequence 354, App	244	5	4.1	176	6	US-10-121-044-98	Sequence 98, Appl
172	5	4.1	121	6	US-10-012-121A-354	Sequence 354, App	245	5	4.1	176	6	US-10-121-047-98	Sequence 98, Appl

246	5	4.1	176	6	US-10-121-054-98	Sequence 98, Appl	319	5	4.1	249	6	US-10-121-058-110	Sequence 110, App
247	5	4.1	176	6	US-10-121-056-98	Sequence 98, Appl	320	5	4.1	249	6	US-10-121-060-110	Sequence 110, App
248	5	4.1	176	6	US-10-121-057-98	Sequence 98, Appl	321	5	4.1	249	6	US-10-121-063-110	Sequence 110, App
249	5	4.1	176	6	US-10-121-058-98	Sequence 98, Appl	322	5	4.1	249	6	US-10-112-267-56	Sequence 56, Appl
250	5	4.1	176	6	US-10-121-060-98	Sequence 98, Appl	323	5	4.1	249	6	US-10-123-108-110	Sequence 110, App
251	5	4.1	176	6	US-10-121-063-98	Sequence 98, Appl	324	5	4.1	249	6	US-10-123-154-110	Sequence 110, App
252	5	4.1	176	6	US-10-123-108-98	Sequence 98, Appl	325	5	4.1	249	6	US-10-123-157-110	Sequence 110, App
253	5	4.1	176	6	US-10-123-154-98	Sequence 98, Appl	326	5	4.1	249	6	US-10-123-157-110	Sequence 110, App
254	5	4.1	176	6	US-10-123-156-98	Sequence 98, Appl	327	5	4.1	249	6	US-10-123-212-110	Sequence 110, App
255	5	4.1	176	6	US-10-123-157-98	Sequence 98, Appl	328	5	4.1	249	6	US-10-123-213-110	Sequence 110, App
256	5	4.1	176	6	US-10-123-212-98	Sequence 98, Appl	329	5	4.1	249	6	US-10-123-109-110	Sequence 110, App
257	5	4.1	176	6	US-10-123-213-98	Sequence 98, Appl	330	5	4.1	249	6	US-10-121-041-110	Sequence 110, App
258	5	4.1	176	6	US-10-123-109-98	Sequence 98, Appl	331	5	4.1	249	6	US-10-121-045-110	Sequence 110, App
259	5	4.1	176	6	US-10-121-041-98	Sequence 98, Appl	332	5	4.1	249	6	US-10-121-046-110	Sequence 110, App
260	5	4.1	176	6	US-10-121-045-98	Sequence 98, Appl	333	5	4.1	249	6	US-10-121-051-110	Sequence 110, App
261	5	4.1	176	6	US-10-121-046-98	Sequence 98, Appl	334	5	4.1	250	6	US-10-121-049-320	Sequence 320, App
262	5	4.1	176	6	US-10-121-051-98	Sequence 98, Appl	335	5	4.1	250	6	US-10-121-050-320	Sequence 320, App
263	5	4.1	179	5	US-09-540-209B-7366	Sequence 7366, Ap	336	5	4.1	250	6	US-10-121-053-320	Sequence 320, App
264	5	4.1	183	6	US-10-106-698-4841	Sequence 4841, Ap	337	5	4.1	250	6	US-10-121-043-320	Sequence 320, App
265	5	4.1	193	5	US-09-573-655B-2345	Sequence 2345, Ap	338	5	4.1	250	6	US-10-121-044-320	Sequence 320, App
266	5	4.1	193	6	US-10-102-806-713	Sequence 713, App	339	5	4.1	250	6	US-10-121-047-320	Sequence 320, App
267	5	4.1	196	5	US-09-990-004A-73	Sequence 73, Appl	340	5	4.1	250	6	US-10-121-054-320	Sequence 320, App
268	5	4.1	198	6	US-10-060-255-79	Sequence 79, Appl	341	5	4.1	250	6	US-10-121-056-320	Sequence 320, App
269	5	4.1	199	5	US-09-540-209B-7450	Sequence 7450, Ap	342	5	4.1	250	6	US-10-121-057-320	Sequence 320, App
270	5	4.1	200	6	US-10-105-931-11	Sequence 11, Appl	343	5	4.1	250	6	US-10-121-058-320	Sequence 320, App
271	5	4.1	202	5	US-09-540-209B-6069	Sequence 6069, Ap	344	5	4.1	250	6	US-10-121-060-320	Sequence 320, App
272	5	4.1	202	5	US-09-540-209B-8896	Sequence 8896, Ap	345	5	4.1	250	6	US-10-121-063-320	Sequence 320, App
273	5	4.1	205	6	US-10-023-171-29	Sequence 29, Appl	346	5	4.1	250	6	US-10-112-267-16	Sequence 16, Appl
274	5	4.1	205	6	US-09-540-209B-7817	Sequence 7817, Ap	347	5	4.1	250	6	US-10-123-108-320	Sequence 320, App
275	5	4.1	206	1	PCT-US02-09921-864	Sequence 864, App	348	5	4.1	250	6	US-10-123-154-320	Sequence 320, App
276	5	4.1	207	1	PCT-US02-09921-658	Sequence 658, App	349	5	4.1	250	6	US-10-123-156-320	Sequence 320, App
277	5	4.1	209	5	US-09-540-209B-5497	Sequence 5497, Ap	350	5	4.1	250	6	US-10-123-157-320	Sequence 320, App
278	5	4.1	211	5	US-09-540-209B-7149	Sequence 7149, Ap	351	5	4.1	250	6	US-10-123-212-320	Sequence 320, App
279	5	4.1	211	5	US-09-540-209B-7708	Sequence 7708, Ap	352	5	4.1	250	6	US-10-123-213-320	Sequence 320, App
280	5	4.1	216	1	PCT-US02-09785-1015	Sequence 1015, Ap	353	5	4.1	250	6	US-10-123-109-320	Sequence 320, App
281	5	4.1	217	6	US-10-105-299-5152	Sequence 5152, Ap	354	5	4.1	250	6	US-10-121-041-320	Sequence 320, App
282	5	4.1	218	6	US-10-105-239-5797	Sequence 5797, Ap	355	5	4.1	250	6	US-10-121-045-320	Sequence 320, App
283	5	4.1	223	1	US-09-895-913A-84	Sequence 84, Appl	356	5	4.1	250	6	US-10-121-046-320	Sequence 320, App
284	5	4.1	224	1	PCT-US02-09921-1101	Sequence 1101, Ap	357	5	4.1	250	6	US-10-121-051-320	Sequence 320, App
285	5	4.1	225	5	US-09-540-209B-6866	Sequence 6866, Ap	358	5	4.1	251	5	US-09-540-209B-8488	Sequence 8488, Ap
286	5	4.1	226	6	US-10-106-698-6008	Sequence 6008, Ap	359	5	4.1	251	5	US-09-981-566A-51	Sequence 51, Appl
287	5	4.1	227	6	US-10-103-313-468	Sequence 468, App	360	5	4.1	253	6	US-10-102-627-66	Sequence 66, Appl
288	5	4.1	229	5	US-09-540-209B-9700	Sequence 9700, Ap	361	5	4.1	253	6	US-10-114-666-454	Sequence 454, App
289	5	4.1	231	6	US-10-106-698-4582	Sequence 4582, Ap	362	5	4.1	255	7	US-60-370-796-13	Sequence 13, Appl
290	5	4.1	232	6	US-10-106-698-5299	Sequence 5299, Ap	363	5	4.1	257	5	US-09-813-453A-13	Sequence 13, Appl
291	5	4.1	237	1	PCT-US02-09921-773	Sequence 773, App	364	5	4.1	260	5	US-09-989-930-2	Sequence 2, Appl
292	5	4.1	237	5	US-09-540-209B-7829	Sequence 7829, Ap	365	5	4.1	261	5	US-09-540-209B-5752	Sequence 5752, Ap
293	5	4.1	239	5	US-09-540-209B-7225	Sequence 7225, Ap	366	5	4.1	261	6	US-10-006-063A-402	Sequence 402, App
294	5	4.1	239	5	US-09-990-004A-65	Sequence 65, Appl	367	5	4.1	261	6	US-10-006-117A-402	Sequence 402, App
295	5	4.1	240	5	US-09-573-655B-937	Sequence 937, App	368	5	4.1	261	6	US-10-006-130A-402	Sequence 402, App
296	5	4.1	240	5	US-09-540-209B-6433	Sequence 6433, Ap	369	5	4.1	261	6	US-10-006-172A-402	Sequence 402, App
297	5	4.1	241	6	US-10-112-267-64	Sequence 64, Appl	370	5	4.1	261	6	US-10-006-768A-402	Sequence 402, App
298	5	4.1	242	6	US-10-112-267-63	Sequence 63, Appl	371	5	4.1	261	6	US-10-017-527A-402	Sequence 402, App
299	5	4.1	243	6	US-10-112-267-62	Sequence 62, Appl	372	5	4.1	261	6	US-10-017-610A-402	Sequence 402, App
300	5	4.1	244	6	US-10-112-267-61	Sequence 61, Appl	373	5	4.1	261	6	US-10-006-041A-402	Sequence 402, App
301	5	4.1	245	6	US-10-112-267-60	Sequence 60, Appl	374	5	4.1	261	6	US-10-006-818A-402	Sequence 402, App
302	5	4.1	246	6	US-09-573-655B-23	Sequence 23, Appl	375	5	4.1	261	6	US-10-012-121A-402	Sequence 402, App
303	5	4.1	246	6	US-10-112-267-59	Sequence 59, Appl	376	5	4.1	261	6	US-10-015-386A-402	Sequence 402, App
304	5	4.1	247	6	US-10-112-267-58	Sequence 58, Appl	377	5	4.1	261	6	US-10-015-387A-402	Sequence 402, App
305	5	4.1	247	6	US-10-120-414-79	Sequence 79, Appl	378	5	4.1	261	6	US-10-121-049-546	Sequence 546, App
306	5	4.1	248	6	US-10-103-196-15	Sequence 15, Appl	379	5	4.1	261	6	US-10-121-050-546	Sequence 546, App
307	5	4.1	248	6	US-10-112-267-57	Sequence 57, Appl	380	5	4.1	261	6	US-10-121-053-546	Sequence 546, App
308	5	4.1	249	1	PCT-US02-10421-2897	Sequence 2897, Ap	381	5	4.1	261	6	US-10-121-043-546	Sequence 546, App
309	5	4.1	249	6	US-10-112-699-2897	Sequence 2897, Ap	382	5	4.1	261	6	US-10-121-044-546	Sequence 546, App
310	5	4.1	249	6	US-10-121-049-110	Sequence 110, App	383	5	4.1	261	6	US-10-121-047-546	Sequence 546, App
311	5	4.1	249	6	US-10-121-050-110	Sequence 110, App	384	5	4.1	261	6	US-10-121-054-546	Sequence 546, App
312	5	4.1	249	6	US-10-121-053-110	Sequence 110, App	385	5	4.1	261	6	US-10-121-056-546	Sequence 546, App
313	5	4.1	249	6	US-10-121-043-110	Sequence 110, App	386	5	4.1	261	6	US-10-121-057-546	Sequence 546, App
314	5	4.1	249	6	US-10-121-044-110	Sequence 110, App	387	5	4.1	261	6	US-10-121-058-546	Sequence 546, App
315	5	4.1	249	6	US-10-121-047-110	Sequence 110, App	388	5	4.1	261	6	US-10-121-060-546	Sequence 546, App
316	5	4.1	249	6	US-10-121-054-110	Sequence 110, App	389	5	4.1	261	6	US-10-121-063-546	Sequence 546, App
317	5	4.1	249	6	US-10-121-056-110	Sequence 110, App	390	5	4.1	261	6	US-10-123-108-546	Sequence 546, App
318	5	4.1	249	6	US-10-121-057-110	Sequence 110, App	391	5	4.1	261	6	US-10-123-134-546	Sequence 546, App

392	5	4.1	261	6	US-10-123-156-546	Sequence 546, App	465	5	4.1	305	5	US-09-540-209B-10050	Sequence 10050, A
393	5	4.1	261	6	US-10-123-157-546	Sequence 546, App	466	5	4.1	305	5	US-09-990-004A-188	Sequence 188, App
394	5	4.1	261	6	US-10-123-212-546	Sequence 546, App	467	5	4.1	305	6	US-10-106-698-4414	Sequence 4414, Ap
395	5	4.1	261	6	US-10-123-213-546	Sequence 546, App	468	5	4.1	307	5	US-09-743-207-12	Sequence 12, Appl
396	5	4.1	261	6	US-10-123-109-546	Sequence 546, App	469	5	4.1	308	5	US-09-981-566A-75	Sequence 75, Appl
397	5	4.1	261	6	US-10-121-041-546	Sequence 546, App	470	5	4.1	310	5	US-09-540-209B-5549	Sequence 5549, Ap
398	5	4.1	261	6	US-10-121-045-546	Sequence 546, App	471	5	4.1	311	5	US-09-907-218-55	Sequence 55, Appl
399	5	4.1	261	6	US-10-121-046-546	Sequence 546, App	472	5	4.1	311	6	US-10-106-698-5688	Sequence 5688, Ap
400	5	4.1	261	6	US-10-121-051-546	Sequence 546, App	473	5	4.1	312	7	US-60-372-508-12	Sequence 12, Appl
401	5	4.1	262	6	US-10-114-666-457	Sequence 457, App	474	5	4.1	313	1	PCT-US02-03635-40	Sequence 40, Appl
402	5	4.1	263	5	US-09-540-209B-6940	Sequence 6940, App	475	5	4.1	313	6	US-10-121-746-81	Sequence 81, Appl
403	5	4.1	265	5	US-09-540-209B-5433	Sequence 5433, App	476	5	4.1	314	6	US-10-032-106-10	Sequence 10, Appl
404	5	4.1	265	5	US-09-540-209B-6712	Sequence 6712, App	477	5	4.1	315	1	PCT-US02-09923-10	Sequence 10, Appl
405	5	4.1	266	1	PCT-US02-09921-804	Sequence 804, Appl	478	5	4.1	315	5	US-09-965-422-20	Sequence 20, Appl
406	5	4.1	266	6	US-10-089-720-3	Sequence 3, Appl	479	5	4.1	315	5	US-09-965-422-22	Sequence 22, Appl
407	5	4.1	269	6	US-10-103-313-319	Sequence 319, App	480	5	4.1	315	5	US-09-965-422-24	Sequence 24, Appl
408	5	4.1	272	5	US-09-540-209B-6270	Sequence 6270, App	481	5	4.1	316	1	PCT-US02-01339-12	Sequence 12, Appl
409	5	4.1	273	6	US-10-106-698-4937	Sequence 4937, App	482	5	4.1	316	5	US-09-978-403A-137	Sequence 137, App
410	5	4.1	273	6	US-10-121-049-540	Sequence 540, App	483	5	4.1	316	5	US-09-978-544A-137	Sequence 137, App
411	5	4.1	273	6	US-10-121-050-540	Sequence 540, App	484	5	4.1	316	5	US-09-978-681A-137	Sequence 137, App
412	5	4.1	273	6	US-10-121-053-540	Sequence 540, App	485	5	4.1	316	5	US-09-978-757A-137	Sequence 137, App
413	5	4.1	273	6	US-10-121-043-540	Sequence 540, App	486	5	4.1	316	5	US-09-978-757A-137	Sequence 137, App
414	5	4.1	273	6	US-10-121-044-540	Sequence 540, App	487	5	4.1	316	5	US-09-999-831A-137	Sequence 137, App
415	5	4.1	273	6	US-10-121-047-540	Sequence 540, App	488	5	4.1	316	5	US-09-540-209B-6651	Sequence 6651, Ap
416	5	4.1	273	6	US-10-121-054-540	Sequence 540, App	489	5	4.1	316	5	US-09-540-209B-6651	Sequence 6651, Ap
417	5	4.1	273	6	US-10-121-056-540	Sequence 540, App	490	5	4.1	316	5	US-09-990-004A-62	Sequence 62, Appl
418	5	4.1	273	6	US-10-121-057-540	Sequence 540, App	491	5	4.1	316	6	US-10-013-921A-137	Sequence 137, App
419	5	4.1	273	6	US-10-121-058-540	Sequence 540, App	492	5	4.1	316	6	US-10-013-929A-137	Sequence 137, App
420	5	4.1	273	6	US-10-121-060-540	Sequence 540, App	493	5	4.1	316	6	US-10-013-918A-137	Sequence 137, App
421	5	4.1	273	6	US-10-121-063-540	Sequence 540, App	494	5	4.1	316	6	US-10-017-082A-137	Sequence 137, App
422	5	4.1	273	6	US-10-123-109-540	Sequence 540, App	495	5	4.1	317	1	PCT-US02-09921-707	Sequence 707, App
423	5	4.1	273	6	US-10-123-154-540	Sequence 540, App	496	5	4.1	317	5	US-09-540-209B-7157	Sequence 7157, Ap
424	5	4.1	273	6	US-10-123-156-540	Sequence 540, App	497	5	4.1	322	7	US-60-365-384-314	Sequence 314, App
425	5	4.1	273	6	US-10-123-157-540	Sequence 540, App	498	5	4.1	323	5	US-09-540-209B-8468	Sequence 8468, Ap
426	5	4.1	273	6	US-10-123-212-540	Sequence 540, App	499	5	4.1	324	1	PCT-US02-09923-25	Sequence 25, Appl
427	5	4.1	273	6	US-10-123-213-540	Sequence 540, App	500	5	4.1	324	5	US-09-573-655B-2119	Sequence 2119, Ap
428	5	4.1	273	6	US-10-123-109-540	Sequence 540, App	501	5	4.1	326	6	US-10-108-605-19	Sequence 19, Appl
429	5	4.1	273	6	US-10-121-041-540	Sequence 540, App	502	5	4.1	327	1	PCT-US02-03635-39	Sequence 39, Appl
430	5	4.1	273	6	US-10-121-045-540	Sequence 540, App	503	5	4.1	327	6	US-10-125-459-8	Sequence 8, Appl
431	5	4.1	273	6	US-10-121-046-540	Sequence 540, App	504	5	4.1	328	1	PCT-US02-08288-2	Sequence 2, Appl
432	5	4.1	273	6	US-10-121-051-540	Sequence 540, App	505	5	4.1	328	6	US-10-106-698-4635	Sequence 4635, Ap
433	5	4.1	274	1	PCT-US02-09921-978	Sequence 978, App	506	5	4.1	332	5	US-09-540-209B-8282	Sequence 8282, Ap
434	5	4.1	274	6	US-09-540-209B-8195	Sequence 8195, App	507	5	4.1	332	6	US-10-106-698-6370	Sequence 6370, Ap
435	5	4.1	274	6	US-10-121-988-74	Sequence 74, Appl	508	5	4.1	333	5	US-09-573-655B-1256	Sequence 1256, Ap
436	5	4.1	279	5	US-09-573-655B-978	Sequence 978, App	509	5	4.1	334	5	US-09-540-209B-9829	Sequence 9829, Ap
437	5	4.1	279	5	US-09-540-209B-7582	Sequence 7582, App	510	5	4.1	335	5	US-09-540-209B-7085	Sequence 7085, Ap
438	5	4.1	280	6	US-10-115-899-5	Sequence 5, Appl	511	5	4.1	338	5	US-09-312-283B-325	Sequence 325, App
439	5	4.1	280	6	US-10-115-899-8	Sequence 8, Appl	512	5	4.1	338	5	US-09-540-209B-7491	Sequence 7491, Ap
440	5	4.1	281	5	US-09-540-209B-6267	Sequence 6267, App	513	5	4.1	341	5	US-09-540-209B-7542	Sequence 7542, Ap
441	5	4.1	282	1	PCT-US02-09785-815	Sequence 815, App	514	5	4.1	344	5	US-09-540-209B-8052	Sequence 8052, Ap
442	5	4.1	283	5	US-09-540-209B-10359	Sequence 10359, A	515	5	4.1	345	1	PCT-US02-09944-478	Sequence 478, App
443	5	4.1	284	5	US-09-540-209B-7292	Sequence 7292, App	516	5	4.1	345	6	US-10-106-698-6316	Sequence 6316, Ap
444	5	4.1	287	5	US-09-762-154-18	Sequence 18, Appl	517	5	4.1	346	1	PCT-US02-07999-82	Sequence 82, Appl
445	5	4.1	288	5	US-09-540-209B-7740	Sequence 7740, App	518	5	4.1	346	1	PCT-US01-09366A-2	Sequence 2, Appl
446	5	4.1	289	6	US-10-011-585A-167	Sequence 167, App	519	5	4.1	346	1	PCT-US01-09366A-2	Sequence 2, Appl
447	5	4.1	290	1	PCT-US02-10303-23	Sequence 23, Appl	520	5	4.1	347	5	US-09-540-209B-5775	Sequence 5775, Ap
448	5	4.1	290	1	PCT-US02-10371-23	Sequence 23, Appl	521	5	4.1	348	5	US-09-602-777A-436	Sequence 436, App
449	5	4.1	290	5	US-09-540-209B-7640	Sequence 7640, App	522	5	4.1	350	5	US-09-540-209B-9575	Sequence 9575, Ap
450	5	4.1	290	6	US-10-102-806-494	Sequence 494, App	523	5	4.1	350	5	US-09-602-777A-290	Sequence 290, App
451	5	4.1	290	6	US-10-115-609-23	Sequence 23, Appl	524	5	4.1	351	5	US-09-573-655B-1835	Sequence 1835, Ap
452	5	4.1	290	6	US-10-115-609-23	Sequence 23, Appl	525	5	4.1	351	6	US-10-106-698-4697	Sequence 4697, Ap
453	5	4.1	293	5	US-09-635-554-2	Sequence 2, Appl	526	5	4.1	355	5	US-09-540-209B-6354	Sequence 6354, App
454	5	4.1	293	6	US-10-084-971-2	Sequence 10, Appl	527	5	4.1	356	5	US-09-573-655B-303	Sequence 303, App
455	5	4.1	293	7	US-60-372-508-10	Sequence 10, Appl	528	5	4.1	357	7	US-60-365-264-651	Sequence 651, App
456	5	4.1	294	5	US-09-540-209B-6860	Sequence 6860, App	529	5	4.1	358	6	US-10-104-340-2	Sequence 2, Appl
457	5	4.1	295	5	US-09-573-655B-219	Sequence 219, App	530	5	4.1	358	6	US-10-106-698-6181	Sequence 6181, Ap
458	5	4.1	299	5	US-09-540-209B-5571	Sequence 5571, App	531	5	4.1	359	5	US-09-540-209B-5642	Sequence 5642, Ap
459	5	4.1	300	5	US-09-573-655B-394	Sequence 394, App	532	5	4.1	361	1	PCT-US02-09944-570	Sequence 570, App
460	5	4.1	300	5	US-09-573-655B-1582	Sequence 1582, App	533	5	4.1	361	6	US-10-108-605-255	Sequence 255, App
461	5	4.1	302	5	US-09-573-655B-1003	Sequence 1003, App	534	5	4.1	361	6	US-10-106-698-5093	Sequence 5093, Ap
462	5	4.1	303	5	US-09-540-209B-7767	Sequence 7767, App	535	5	4.1	363	1	PCT-US02-09944-412	Sequence 412, App
463	5	4.1	303	5	US-09-540-209B-8459	Sequence 8459, App	536	5	4.1	363	5	US-09-540-209B-7020	Sequence 7020, Ap
464	5	4.1	304	5	US-09-573-655B-102	Sequence 102, App	537	5	4.1	363	6	US-10-006-063A-72	Sequence 72, Appl

538	5	4.1	363	6	US-10-006-117A-72	Sequence 72, Appl	611	5	4.1	435	5	US-09-540-209B-7964	Sequence 7964, Ap
539	5	4.1	363	6	US-10-006-130A-72	Sequence 72, Appl	612	5	4.1	437	5	US-09-540-209B-7669	Sequence 7669, Ap
540	5	4.1	363	6	US-10-006-172A-72	Sequence 72, Appl	613	5	4.1	437	5	US-09-540-209B-9492	Sequence 9492, Ap
541	5	4.1	363	6	US-10-006-768A-72	Sequence 72, Appl	614	5	4.1	438	1	PCT-US01-25881-21	Sequence 21, Appl
542	5	4.1	363	6	US-10-017-527A-72	Sequence 72, Appl	615	5	4.1	439	5	US-09-540-209B-6330	Sequence 6330, Ap
543	5	4.1	363	6	US-10-017-610A-72	Sequence 72, Appl	616	5	4.1	440	5	US-09-743-207-2	Sequence 2, Appl
544	5	4.1	363	6	US-10-006-041A-72	Sequence 72, Appl	617	5	4.1	440	5	US-09-540-209B-6875	Sequence 6875, Ap
545	5	4.1	363	6	US-10-006-018A-72	Sequence 72, Appl	618	5	4.1	444	4	US-08-945-821D-4	Sequence 4, Appl
546	5	4.1	363	6	US-10-012-121A-72	Sequence 72, Appl	619	5	4.1	444	4	US-08-945-821D-6	Sequence 6, Appl
547	5	4.1	363	6	US-10-015-386A-72	Sequence 72, Appl	620	5	4.1	444	4	US-09-573-655B-1255	Sequence 1255, Ap
548	5	4.1	363	6	US-10-015-387A-72	Sequence 72, Appl	621	5	4.1	444	6	US-10-023-839-3	Sequence 3, Appl
549	5	4.1	364	7	US-60-365-264-680	Sequence 680, App	622	5	4.1	446	6	US-10-023-839-5	Sequence 5, Appl
550	5	4.1	372	7	US-60-366-892-14	Sequence 14, Appl	623	5	4.1	446	6	US-10-103-313-326	Sequence 120, App
551	5	4.1	374	5	US-09-540-209B-8992	Sequence 8992, Ap	624	5	4.1	446	6	PCT-US02-09944-751	Sequence 326, App
552	5	4.1	381	5	US-09-540-209B-6324	Sequence 6324, Ap	625	5	4.1	448	1	PCT-US02-09944-751	Sequence 751, App
553	5	4.1	381	5	US-09-540-209B-7389	Sequence 7389, Ap	626	5	4.1	449	5	US-09-540-209B-5270	Sequence 5270, Ap
554	5	4.1	383	6	US-10-108-605-105	Sequence 105, App	627	5	4.1	450	1	PCT-US02-08523-13	Sequence 13, Appl
555	5	4.1	387	6	US-10-106-698-6168	Sequence 6168, Ap	628	5	4.1	450	7	US-60-366-892-15	Sequence 15, Appl
556	5	4.1	387	7	US-60-365-384-539	Sequence 539, App	629	5	4.1	452	5	US-09-540-209B-5473	Sequence 5473, Ap
557	5	4.1	389	5	US-09-573-655B-689	Sequence 689, App	630	5	4.1	452	5	US-09-540-209B-6551	Sequence 6551, Ap
558	5	4.1	389	5	US-09-573-655B-1042	Sequence 1042, Ap	631	5	4.1	453	5	US-09-978-403A-69	Sequence 69, Appl
559	5	4.1	389	5	US-09-573-655B-1762	Sequence 1762, Ap	632	5	4.1	453	5	US-09-978-344A-69	Sequence 69, Appl
560	5	4.1	392	5	US-09-540-209B-6376	Sequence 6376, Ap	633	5	4.1	453	5	US-09-978-681A-69	Sequence 69, Appl
561	5	4.1	392	6	US-10-117-532-10	Sequence 10, Appl	634	5	4.1	453	5	US-09-978-757A-69	Sequence 69, Appl
562	5	4.1	394	6	US-10-117-532-5	Sequence 5, Appl	635	5	4.1	453	5	US-09-978-564A-69	Sequence 69, Appl
563	5	4.1	395	5	US-09-573-655B-1317	Sequence 1317, Ap	636	5	4.1	453	5	US-09-999-831A-69	Sequence 69, Appl
564	5	4.1	396	1	PCT-US02-09921-1113	Sequence 1113, Ap	637	5	4.1	453	5	US-09-999-829A-69	Sequence 69, Appl
565	5	4.1	397	5	US-09-006-428A-2	Sequence 2, Appl	638	5	4.1	453	6	US-10-013-929A-69	Sequence 69, Appl
566	5	4.1	397	5	US-09-006-428A-19	Sequence 19, Appl	639	5	4.1	453	6	US-10-013-929A-69	Sequence 69, Appl
567	5	4.1	399	5	US-09-763-154-90	Sequence 90, Appl	640	5	4.1	453	6	US-10-013-918A-69	Sequence 69, Appl
568	5	4.1	400	5	US-09-540-209B-5896	Sequence 5896, Ap	641	5	4.1	453	6	US-10-017-082A-69	Sequence 69, Appl
569	5	4.1	401	5	US-09-901-556A-3	Sequence 3, Appl	642	5	4.1	453	6	US-10-106-698-5604	Sequence 5604, Ap
570	5	4.1	402	5	US-09-540-209B-9410	Sequence 9410, Ap	643	5	4.1	455	1	PCT-US01-25881-4	Sequence 4, Appl
571	5	4.1	403	1	PCT-US02-07826-149	Sequence 149, App	644	5	4.1	456	1	US-10-107-431-87	Sequence 87, Appl
572	5	4.1	403	5	US-09-573-655B-1452	Sequence 1452, Ap	645	5	4.1	458	1	PCT-US01-25881-3	Sequence 3, Appl
573	5	4.1	403	6	US-10-097-340-149	Sequence 149, App	646	5	4.1	458	1	PCT-US01-25881-27	Sequence 27, Appl
574	5	4.1	404	5	US-09-540-209B-7980	Sequence 7980, Ap	647	5	4.1	458	6	US-10-115-415-4	Sequence 4, Appl
575	5	4.1	405	5	US-09-540-209B-9615	Sequence 9615, Ap	648	5	4.1	458	6	US-10-115-671-4	Sequence 4, Appl
576	5	4.1	405	6	US-10-109-550-2	Sequence 2, Appl	649	5	4.1	458	6	US-10-115-688-4	Sequence 4, Appl
577	5	4.1	406	6	US-10-117-532-4	Sequence 4, Appl	650	5	4.1	458	6	US-10-115-685-4	Sequence 4, Appl
578	5	4.1	407	6	US-10-117-532-2	Sequence 2, Appl	651	5	4.1	458	6	US-10-116-260-4	Sequence 4, Appl
579	5	4.1	408	5	US-09-749-728B-210	Sequence 210, App	652	5	4.1	458	6	US-10-116-561-4	Sequence 4, Appl
580	5	4.1	408	5	US-09-573-655B-210	Sequence 210, App	653	5	4.1	461	5	US-09-978-917A-2	Sequence 2, Appl
581	5	4.1	409	1	PCT-US01-25881-20	Sequence 20, Appl	654	5	4.1	461	5	US-09-997-623-2	Sequence 2, Appl
582	5	4.1	411	5	US-09-749-728B-1	Sequence 1, Appl	655	5	4.1	461	5	PCT-US02-09921-688	Sequence 688, App
583	5	4.1	411	5	US-09-895-913A-292	Sequence 292, App	656	5	4.1	467	5	US-09-540-209B-7672	Sequence 7672, Ap
584	5	4.1	412	5	US-09-573-655B-711	Sequence 711, App	657	5	4.1	467	1	PCT-US02-07826-171	Sequence 171, App
585	5	4.1	412	5	US-09-573-655B-1217	Sequence 1217, Ap	658	5	4.1	469	1	PCT-US02-07826-173	Sequence 173, App
586	5	4.1	415	6	US-10-102-806-437	Sequence 437, App	659	5	4.1	469	5	US-09-573-655B-1089	Sequence 1089, Ap
587	5	4.1	416	5	US-09-006-428A-1	Sequence 1, Appl	660	5	4.1	469	6	US-10-097-340-171	Sequence 171, App
588	5	4.1	416	5	US-09-006-428A-17	Sequence 17, Appl	661	5	4.1	469	6	US-10-097-340-173	Sequence 173, App
589	5	4.1	419	5	US-09-978-917A-4	Sequence 4, Appl	662	5	4.1	471	6	US-10-100-679-96	Sequence 96, Appl
590	5	4.1	419	5	US-09-997-623-4	Sequence 4, Appl	663	5	4.1	476	7	US-60-363-384-574	Sequence 574, App
591	5	4.1	419	5	US-09-540-209B-6424	Sequence 6424, Ap	664	5	4.1	481	5	US-09-540-209B-6068	Sequence 6068, Ap
592	5	4.1	419	5	US-09-540-209B-7719	Sequence 7719, Ap	665	5	4.1	482	6	US-10-106-698-4627	Sequence 4627, Ap
593	5	4.1	420	5	US-09-573-655B-1611	Sequence 1611, Ap	666	5	4.1	484	5	US-09-573-655B-1025	Sequence 1025, Ap
594	5	4.1	420	5	US-09-573-655B-2264	Sequence 2264, Ap	667	5	4.1	487	5	US-09-573-655B-1580	Sequence 1580, Ap
595	5	4.1	420	5	US-09-540-209B-8311	Sequence 8311, Ap	668	5	4.1	488	6	US-10-109-310-15	Sequence 15, Appl
596	5	4.1	422	5	US-09-540-209B-5265	Sequence 5265, Ap	669	5	4.1	489	1	PCT-US02-10818-15	Sequence 15, Appl
597	5	4.1	423	6	US-10-100-679-95	Sequence 95, Appl	670	5	4.1	489	5	US-09-991-150-138	Sequence 138, App
598	5	4.1	423	6	US-10-107-431-31	Sequence 31, Appl	671	5	4.1	490	6	US-10-105-931-26	Sequence 26, Appl
599	5	4.1	424	1	PCT-US02-09944-705	Sequence 705, App	672	5	4.1	491	5	US-09-863-776-34	Sequence 34, Appl
600	5	4.1	424	5	US-09-573-655B-1484	Sequence 1484, Ap	673	5	4.1	495	5	US-09-915-181A-7	Sequence 7, Appl
601	5	4.1	425	6	US-10-113-113-2	Sequence 2, Appl	674	5	4.1	496	1	PCT-US02-09944-440	Sequence 440, App
602	5	4.1	426	5	US-09-540-209B-5807	Sequence 5807, Ap	675	5	4.1	496	6	US-10-067-741-46	Sequence 46, Appl
603	5	4.1	426	5	US-09-540-209B-6010	Sequence 6010, Ap	676	5	4.1	497	5	US-09-868-300-10	Sequence 10, Appl
604	5	4.1	427	7	US-60-366-892-38	Sequence 38, Appl	677	5	4.1	498	5	US-09-573-655B-512	Sequence 512, App
605	5	4.1	429	5	US-09-573-655B-1009	Sequence 1009, Ap	678	5	4.1	498	5	US-09-573-655B-593	Sequence 593, App
606	5	4.1	429	5	US-09-743-207-8	Sequence 8, Appl	679	5	4.1	505	5	US-09-573-655B-382	Sequence 382, App
607	5	4.1	432	5	US-09-573-655B-1198	Sequence 1198, Ap	680	5	4.1	507	7	US-60-368-184-3	Sequence 3, Appl
608	5	4.1	433	6	US-10-102-806-463	Sequence 463, App	681	5	4.1	507	7	US-60-366-892-41	Sequence 41, Appl
609	5	4.1	434	1	PCT-US02-07826-73	Sequence 73, Appl	682	5	4.1	510	6	US-10-112-857-15	Sequence 15, Appl
610	5	4.1	434	6	US-10-097-340-73	Sequence 73, Appl	683	5	4.1	511	7	US-60-366-892-42	Sequence 42, Appl

684	5	4.1	514	5	US-09-540-209B-9965	Sequence 9965, Ap	757	607	6	US-10-121-051-344	Sequence 344, App
685	5	4.1	516	1	PCT-US02-09944-525	Sequence 525, App	758	608	5	US-09-540-209B-8786	Sequence 8786, Ap
686	5	4.1	516	5	US-09-573-655B-193	Sequence 193, App	759	613	1	PCT-US02-09944-680	Sequence 680, App
687	5	4.1	516	5	US-09-573-655B-255	Sequence 255, App	760	615	6	US-10-112-178-2	Sequence 2, Appli
688	5	4.1	516	5	US-09-573-655B-1516	Sequence 1516, Ap	761	615	6	US-10-112-178-4	Sequence 4, Appli
689	5	4.1	516	5	US-09-573-655B-1746	Sequence 1746, Ap	762	619	5	US-09-573-655B-2391	Sequence 2391, Ap
690	5	4.1	516	5	US-09-573-655B-1860	Sequence 1860, Ap	763	625	7	US-60-365-264-649	Sequence 649, App
691	5	4.1	519	5	US-09-540-209B-6278	Sequence 6278, Ap	764	626	6	US-10-121-235-21	Sequence 21, Appli
692	5	4.1	524	5	US-09-914-543-28	Sequence 28, Appl	765	628	1	PCT-US01-13240-5	Sequence 5, Appli
693	5	4.1	525	5	US-09-972-211-30	Sequence 30, Appl	766	632	6	US-10-041-007-22	Sequence 22, Appl
694	5	4.1	525	5	US-09-972-211-32	Sequence 32, Appl	767	632	5	US-09-540-209B-8469	Sequence 8469, Ap
695	5	4.1	525	5	US-09-972-211-34	Sequence 34, Appl	768	633	5	US-09-540-209B-7938	Sequence 7938, Ap
696	5	4.1	525	5	US-09-972-211-36	Sequence 36, Appl	769	634	5	US-09-602-777A-272	Sequence 272, App
697	5	4.1	525	5	US-09-972-211-38	Sequence 38, Appl	770	634	5	US-09-540-209B-8038	Sequence 8038, Ap
698	5	4.1	525	5	US-09-972-211-40	Sequence 40, Appl	771	635	5	US-09-540-209B-7963	Sequence 7963, Ap
699	5	4.1	525	5	US-09-972-211-103	Sequence 103, App	772	638	5	US-09-540-209B-7940	Sequence 7940, Ap
700	5	4.1	525	5	US-09-972-211-104	Sequence 104, App	773	640	5	US-09-540-209B-7940	Sequence 2022, Ap
701	5	4.1	525	5	US-09-972-211-105	Sequence 105, App	774	641	5	US-09-573-655B-2022	Sequence 44, Appl
702	5	4.1	525	5	US-09-972-211-105	Sequence 105, App	775	642	5	US-09-602-777A-44	Sequence 50, Appl
703	5	4.1	526	5	US-09-366-892-31	Sequence 31, Appl	776	647	5	US-09-991-262-50	Sequence 7045, Ap
704	5	4.1	527	6	US-10-102-806-703	Sequence 703, App	777	649	5	US-09-540-209B-7045	Sequence 10379, A
705	5	4.1	527	7	US-09-366-892-57	Sequence 57, Appl	778	650	5	US-09-540-209B-10379	Sequence 294, App
706	5	4.1	534	1	PCT-US02-06912-7	Sequence 7, Appli	779	650	7	US-60-365-264-294	Sequence 294, App
707	5	4.1	535	7	US-09-366-892-56	Sequence 56, Appl	780	651	7	US-60-368-671-116	Sequence 116, App
708	5	4.1	536	7	US-09-366-892-30	Sequence 30, Appl	781	651	7	US-60-371-420-116	Sequence 116, App
709	5	4.1	537	1	PCT-US02-06912-5	Sequence 5, Appli	782	651	5	US-09-573-655B-1989	Sequence 1989, Ap
710	5	4.1	537	1	PCT-US02-09944-534	Sequence 534, App	783	657	5	US-09-868-677-12	Sequence 12, Appl
711	5	4.1	537	5	US-09-602-777A-46	Sequence 46, Appl	784	667	5	US-09-540-209B-5434	Sequence 5434, Ap
712	5	4.1	540	5	US-09-540-209B-7868	Sequence 7868, Ap	785	669	5	US-09-573-655B-2160	Sequence 2160, Ap
713	5	4.1	540	5	US-09-847-637B-6	Sequence 6, Appli	786	669	5	US-09-573-655B-2198	Sequence 2198, Ap
714	5	4.1	541	6	US-10-100-679-97	Sequence 97, Appl	787	670	6	US-10-106-698-6282	Sequence 6282, Ap
715	5	4.1	543	1	PCT-US02-09944-685	Sequence 685, App	788	675	5	US-09-573-655B-1087	Sequence 1087, Ap
716	5	4.1	543	7	US-09-366-892-68	Sequence 68, Appl	789	678	5	US-09-991-262-52	Sequence 52, Appl
717	5	4.1	544	5	US-09-573-655B-1489	Sequence 1489, Ap	790	678	6	US-09-895-913A-4	Sequence 4, Appli
718	5	4.1	549	5	US-09-573-655B-1671	Sequence 1671, Ap	791	681	1	PCT-US02-10764-20	Sequence 20, Appl
719	5	4.1	554	5	US-09-540-209B-6607	Sequence 6607, Ap	792	681	1	PCT-US02-10764-24	Sequence 24, Appl
720	5	4.1	556	5	US-09-868-300-2	Sequence 2, Appli	793	681	5	US-09-540-209B-6218	Sequence 6218, Ap
721	5	4.1	556	5	US-09-868-300-2	Sequence 2, Appli	794	683	5	US-09-868-677-10	Sequence 10, Appl
722	5	4.1	559	6	US-10-106-275-2	Sequence 536, App	795	685	1	PCT-US02-10764-43	Sequence 43, Appl
723	5	4.1	579	5	US-09-990-004A-185	Sequence 2, Appli	796	685	1	PCT-US02-10764-45	Sequence 45, Appl
724	5	4.1	582	6	US-10-100-679-79	Sequence 79, Appl	797	685	1	PCT-US02-10764-47	Sequence 47, Appl
725	5	4.1	582	6	US-10-100-679-80	Sequence 80, Appl	798	689	1	PCT-US02-10764-221	Sequence 221, App
726	5	4.1	582	6	US-10-100-679-81	Sequence 81, Appl	799	689	6	US-10-097-340-221	Sequence 221, App
727	5	4.1	584	5	US-09-902-525-33	Sequence 33, Appl	800	692	1	PCT-US02-10764-16	Sequence 16, Appl
728	5	4.1	586	5	US-09-540-209B-7381	Sequence 7381, Ap	801	692	1	PCT-US02-10764-22	Sequence 22, Appl
729	5	4.1	587	5	US-09-573-655B-811	Sequence 811, App	802	700	5	US-09-573-655B-1802	Sequence 1802, Ap
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734	5	4.1	607	5	US-09-573-655B-1086	Sequence 1086, Ap	807	722	1	PCT-US02-10812-12	Sequence 12, Appl
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736	5	4.1	607	6	US-10-121-050-344	Sequence 344, App	809	732	5	US-09-573-655B-2355	Sequence 2355, Ap
737	5	4.1	607	6	US-10-121-053-344	Sequence 344, App	810	740	5	US-09-540-209B-8427	Sequence 8427, Ap
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739	5	4.1	607	6	US-10-121-043-344	Sequence 344, App	812	745	7	US-09-540-209B-8524	Sequence 8524, Ap
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741	5	4.1	607	6	US-10-121-043-344	Sequence 344, App	814	746	6	US-10-041-007-39	Sequence 39, Appl
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743	5	4.1	607	6	US-10-121-056-344	Sequence 344, App	816	754	5	US-09-573-655B-925	Sequence 925, App
744	5	4.1	607	6	US-10-121-057-344	Sequence 344, App	817	754	5	US-09-573-655B-1187	Sequence 1187, Ap
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746	5	4.1	607	6	US-10-121-060-344	Sequence 344, App	819	760	5	US-09-540-209B-6609	Sequence 6609, Ap
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749	5	4.1	607	6	US-10-123-154-344	Sequence 344, App	822	770	5	US-09-540-209B-8700	Sequence 8700, Ap
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832	4.1	802	7	US-60-366-892-29	Sequence 29, Appl	905	4.1	953	6	US-09-540-209B-8639	Sequence 8639, Ap
833	4.1	807	7	US-60-371-507-8	Sequence 8, Appl	906	4.1	953	6	US-10-105-931-8	Sequence 8, Appl
834	4.1	807	5	US-09-540-209B-6963	Sequence 6963, Ap	907	4.1	970	5	US-09-573-655B-1537	Sequence 1537, Ap
835	4.1	810	5	US-09-573-655B-1358	Sequence 1358, Ap	908	4.1	971	5	US-09-419-291A-2	Sequence 2, Appl
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838	4.1	814	6	US-09-540-209B-9513	Sequence 9513, Ap	911	4.1	986	5	US-09-540-209B-10025	Sequence 10025, A
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841	4.1	819	5	US-09-540-209B-8521	Sequence 8521, Ap	914	4.1	1005	1	PCT-US02-10133-2	Sequence 2, Appl
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844	4.1	830	5	US-09-540-209B-8070	Sequence 8070, Ap	917	4.1	1013	5	US-09-573-655B-1017	Sequence 1017, Ap
845	4.1	832	5	US-09-540-209B-8034	Sequence 8034, Ap	918	4.1	1016	5	US-10-121-049-198	Sequence 198, Ap
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863	4.1	856	5	US-09-573-655B-1218	Sequence 1218, Ap	936	4.1	1024	6	US-10-123-213-198	Sequence 198, Ap
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867	4.1	877	5	US-10-067-457-1	Sequence 1, Appl	940	4.1	1024	6	US-10-121-046-198	Sequence 198, Ap
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871	4.1	893	7	US-60-365-264-253	Sequence 253, Ap	944	4.1	1035	5	US-09-540-209B-7322	Sequence 7322, Ap
872	4.1	897	5	US-09-914-543-4	Sequence 44, Appl	945	4.1	1035	5	US-09-573-655B-2417	Sequence 2417, Ap
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874	4.1	911	1	PCT-US02-06415-8	Sequence 8, Appl	947	4.1	1042	6	US-10-097-340-83	Sequence 83, Appl
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879	4.1	941	1	PCT-US02-09785-577	Sequence 577, Ap	952	4.1	1052	5	US-09-573-655B-654	Sequence 654, Ap
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882	4.1	941	6	US-10-121-050-464	Sequence 464, Ap	955	4.1	1071	5	US-09-573-655B-2399	Sequence 2399, Ap
883	4.1	941	6	US-10-121-053-464	Sequence 464, Ap	956	4.1	1084	5	US-09-573-655B-7962	Sequence 7962, Ap
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885	4.1	941	6	US-10-121-044-464	Sequence 464, Ap	958	4.1	1092	1	PCT-US02-10055-1858	Sequence 1858, Ap
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895	4.1	941	6	US-10-123-156-464	Sequence 464, Ap	968	4.1	1163	1	PCT-US02-10824-116	Sequence 4, Appl
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898	4.1	941	6	US-10-123-213-464	Sequence 464, Ap	971	4.1	1175	5	PCT-US02-10055-1856	Sequence 1856, Ap
899	4.1	941	6	US-10-123-109-464	Sequence 464, Ap	972	4.1	1202	1	US-10-102-524-1856	Sequence 1856, Ap
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Sequence 2199, Ap
Sequence 9511, Ap
Sequence 211, App
Sequence 7929, Ap
Sequence 8, Appl1
Sequence 2, Appl1
Sequence 2089, Ap
Sequence 158, App
Sequence 95, Appl
Sequence 35, Appl
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Sequence 213, App
Sequence 237, App
Sequence 784, App
Sequence 48, Appl
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Sequence 1841, Ap
Sequence 5708, Ap
Sequence 10, Appl
Sequence 469, App
Sequence 1764, Ap
Sequence 57, Appl
Sequence 1145, Ap

Best Local Similarity 100.0%; Pred. No. 6.1e-60;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRIMLFTAILAFSLAQSGAVCKEPEQEVVPGGGRKRDPLDYQLLQRLFKSHSSLEGL 60

QY 61 LKALSQ 66
Db 61 LKALSQ 66

RESULT 2
US-10-119-480-108
; Sequence 108, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 108
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-119-480-108

Query Match 54.5%; Score 66; DB 6; Length 135;
Best Local Similarity 100.0%; Pred. No. 6.1e-60;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 LKALSQ 66
Db 61 LKALSQ 66

RESULT 3
PCT-US02-10788-25
; Sequence 25, Application PC/TUS0210788
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Antibodies inhibiting autoimmune disease
; FILE REFERENCE: 1361.005W01
; CURRENT APPLICATION NUMBER: PCT/US02/10788
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens

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Sequence 2199, Ap
Sequence 9511, Ap
Sequence 211, App
Sequence 7929, Ap
Sequence 8, Appl1
Sequence 2, Appl1
Sequence 2089, Ap
Sequence 158, App
Sequence 95, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 213, App
Sequence 237, App
Sequence 784, App
Sequence 48, Appl
Sequence 2, Appl1
Sequence 1841, Ap
Sequence 5708, Ap
Sequence 10, Appl
Sequence 469, App
Sequence 1764, Ap
Sequence 57, Appl
Sequence 1145, Ap

Sequence 359, Application US/09991150
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C48
; CURRENT APPLICATION NUMBER: US/09/991,150
; CURRENT FILING DATE: 2001-11-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 532
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; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-150-359

Query Match 54.5%; Score 66; DB 5; Length 135;

PCT-US02-10788-25

Query Match 5.0%; Score 6; DB 1; Length 17;
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 SLAQSF 15

RESULT 4
US-09-710-058A-30
; Sequence 30, Application US/09710058A
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Peelle, Beau
; TITLE OF INVENTION: METHODS AND COMPOSITIONS COMPRISING RENILLA GFP
; FILE REFERENCE: A-68531-1/RMS/CYO
; CURRENT APPLICATION NUMBER: US/09/710,058A
; CURRENT FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/164,592
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.1
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US-09-710-058A-30

Query Match 5.0%; Score 6; DB 5; Length 26;
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RESULT 5
US-10-043-074-19
; Sequence 19, Application US/10043074
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Yu, Pei Wen
; APPLICANT: Lorens, James
; TITLE OF INVENTION: SHUTTLE VECTORS
; FILE REFERENCE: A66252-1/DJB/DAV
; CURRENT APPLICATION NUMBER: US/10/043,074
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,827
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/133,949
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 43
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; SEQ ID NO 19
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: palmitoylated
; PUBLICATION INFORMATION:
; JOURNAL: J. Biol. Chem.
; VOLUME: 269
; PAGES: 27791-27791
; DATE: 1994
US-10-043-074-19

Query Match 5.0%; Score 6; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LLQRLF 51
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Db 1 LLQRLF 6

RESULT 6
US-10-103-295-163
; Sequence 163, Application US/10103295
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P2
; CURRENT APPLICATION NUMBER: US/10/103,295
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: PCT/US01/29871
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/00911
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/234,925
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 09/482,273
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: PCT/US99/15849
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,922
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,956
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-295-163

Query Match 5.0%; Score 6; DB 6; Length 63;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 SLEGLL 61
| | | | |
Db 26 SLEGLL 31

RESULT 7
US-09-540-209B-7680
; Sequence 7680, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
; FILE REFERENCE: 2709.1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7680
; LENGTH: 84
; TYPE: PRT
; ORGANISM: B.fragilis
US-09-540-209B-7680

Query Match 5.0%; Score 6; DB 5; Length 84;
Best Local Similarity 100.0%; Pred. No. 19;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 FGAVCK 24
|||||
Db 15 FGAVCK 20

RESULT 8

US-09-990-004A-166
; Sequence 166, Application US/09990004A
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; TITLE OF INVENTION: Methods for Modulating Cellular Development and Programmed Cell Death
; FILE REFERENCE: 11000.1038c1
; CURRENT APPLICATION NUMBER: US/09/990,004A
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/327,373
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 166
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-990-004A-166

Query Match 5.0%; Score 6; DB 5; Length 96;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 GLLKAL 64
|||||
Db 76 GLLKAL 81

RESULT 9

US-10-106-698-8430
; Sequence 8430, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 8430
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-8430

Query Match 5.0%; Score 6; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 LQRLFK 52
|||||
Db 51 LQRLFK 56

RESULT 10

US-09-990-004A-77
; Sequence 77, Application US/09990004A
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; TITLE OF INVENTION: Methods for Modulating Cellular Development and Programmed Cell Death
; FILE REFERENCE: 11000.1038c1
; CURRENT APPLICATION NUMBER: US/09/990,004A
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/327,373
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-990-004A-77

Query Match 5.0%; Score 6; DB 5; Length 110;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ILAFSL 15
|||||
Db 75 ILAFSL 80

RESULT 11

PCT-US02-10788-11
; Sequence 11, Application PC/TUS0210788
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Antibodies Inhibiting autoimmune disease
; FILE REFERENCE: 1361.005W01
; CURRENT APPLICATION NUMBER: PCT/US02/10788
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-10788-11

Query Match 5.0%; Score 6; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 SLAQSF 19
|||||
Db 52 SLAQSF 57

RESULT 12

US-10-103-295-259
; Sequence 259, Application US/10103295
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P2
; CURRENT APPLICATION NUMBER: US/10/103,295
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: PCT/US01/29871

; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/00911
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/234,925
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 09/482,273
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: PCT/US99/15849
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,922
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,956
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 259
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-295-259

Query Match 5.0%; Score 6; DB 6; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 SLEGLL 61
| | | | |
Db 85 SLEGLL 90

RESULT 13
US-09-990-004A-76
; Sequence 76, Application US/099900004A
; GENERAL INFORMATION:
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Methods for Modulating Cellular Development and Programmed Cell De
; FILE REFERENCE: 11000.1038c1
; CURRENT APPLICATION NUMBER: US/09/990,004A
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/327,373
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-990-004A-76

Query Match 5.0%; Score 6; DB 5; Length 136;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ILAFSL 15
| | | | |
Db 76 ILAFSL 81

RESULT 14
US-09-540-209B-7831
; Sequence 7831, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FRA
; FILE REFERENCE: 2709,1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7831
; LENGTH: 138
; TYPE: PRT
; ORGANISM: B.fragilis
US-09-540-209B-7831

Query Match 5.0%; Score 6; DB 5; Length 138;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LFTAIL 11
| | | | |
Db 87 LFTAIL 92

RESULT 15
US-10-102-806-795
; Sequence 795, Application US/10102806
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 795
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (19)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (23)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (33)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (39)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (49)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (54)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (64)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE

LOCATION: (71)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (76)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (78)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (81)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (83)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (87)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (88)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (89)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (93)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (100)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (107)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (110)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (112)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (117)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (123)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (127)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (136)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-795

Query Match 5.0%; Score 6; DB 6; Length 144;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 GLKAL 64
Db 101 GLKAL 106

Search completed: May 3, 2002, 16:40:05
Job time: 73 sec

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OM protein - protein search, using sw model

Run on: May 3, 2002, 12:20:43 ; Search time 23.81 Seconds
(without alignments)
376.433 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 613
Sequence: 1 MRIMLLFTAILAFSLAQSGF.....DVNQENVPFGLKYPYPRAE 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	610	99.5	121	19 AAW75212	Human secreted pro
2	610	99.5	121	20 AAW97213	A human zneurokl p
3	610	99.5	121	20 AAW74413	HPMB091 protein se
4	610	99.5	121	22 AAB2380	Human neurokinin B
5	609	99.3	121	19 AAW75228	Human secreted pro
6	592.5	96.7	122	20 AAW96144	Human preprotachyk
7	487	79.4	135	21 AAB33445	Human PRO1155 prot
8	487	79.4	135	21 AAB66739	Membrane-bound pro
9	487	79.4	135	22 AAB65262	Human PRO1155 (UNQ
10	407.5	66.5	126	20 AAW96145	Bovine preprotachy
11	344.5	56.2	116	20 AAW96146	Rat preprotachykin

12	261.5	42.7	92	20	AAW97214	A murine homologue
13	247	40.3	51	20	AAW12634	Human 5' EST seque
14	190	31.0	36	19	AAW75249	Fragment of human
15	190	31.0	39	19	AAW74414	HPMB091 protein se
16	77	12.6	15	19	AAW75250	Fragment of human
17	75.5	12.3	195	22	AAG50444	C glutamicum prote
18	71.5	11.7	597	21	AAG25257	Arabidopsis thalia
19	71.5	11.7	598	21	AAG45725	Arabidopsis thalia
20	71.5	11.7	602	21	AAG45724	Arabidopsis thalia
21	71.5	11.7	604	21	AAG25256	Arabidopsis thalia
22	69	11.3	863	13	AAW22357	Carrot aspartokina
23	69	11.3	863	20	AAW75440	Carrot aspartokina
24	68.5	11.2	653	22	AAB93188	Human protein sequ
25	68.5	11.2	704	22	AAB92702	Human protein sequ
26	68	11.1	571	21	AAG30502	Arabidopsis thalia
27	68	11.1	778	21	AAG30501	Arabidopsis thalia
28	68	11.1	808	21	AAG30500	Arabidopsis thalia
29	67.5	11.0	382	17	AAW05322	Human mucosal addr
30	67.5	11.0	382	18	AAW02069	Human MadCAM-1 pro
31	66.5	10.8	2034	20	AAW06300	Human activated ca
32	66.5	10.8	2353	20	AAW06298	Human activated ca
33	66.5	10.8	2353	20	AAW06299	Human activated ca
34	66	10.8	156	22	AAB63675	Human gastric canc
35	66	10.8	343	19	AAW42448	C. heterostrophus
36	65.5	10.7	911	12	AAW15355	Human erythrocyte
37	65.5	10.7	911	20	AAW90263	A. tigrinum AEI pr
38	65.5	10.7	911	22	AAB46914	Human erythrocyte
39	64.5	10.5	647	18	AAW00926	Human cyclin D1-hu
40	64.5	10.5	647	19	AAW74575	Human cyclin D1-cy
41	64.5	10.5	705	18	AAW18573	Human cyclin D1-hu
42	64.5	10.5	705	19	AAW74574	Human cyclin D1-cy
43	64.5	10.5	1005	20	AAW39355	Human 53BP2 protei
44	64.5	10.5	1374	19	AAW69753	Herpes simplex vir
45	64	10.4	562	21	AAW16029	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAW75212
ID AAW75212 standard; Protein; 121 AA.
XX
AC AAW75212;
DT 29-JAN-1999 (first entry)
DE Human secreted protein encoded by gene 17 clone HPMB091.
XX
Human; secreted protein; fusion protein; gene therapy; protein therapy;
diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
developmental abnormality; foetal deficiency; blood; allergy; renal;
immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
Homo sapiens.
XX
PN W09840483-A2.
XX
17-SEP-1998.
XX
12-MAR-1998; 98WO-US04858.
XX
19-DEC-1997; 97US-0068368.
PR 14-MAR-1997; 97US-0040710.
PR 14-MAR-1997; 97US-0040762.
PR 30-MAY-1997; 97US-0048100.
PR 30-MAY-1997; 97US-0048189.
PR 30-MAY-1997; 97US-0048357.
PR 30-MAY-1997; 97US-0050934.

PF 26-JUN-1998; 98EP-0305066.
XX
PR 14-JUL-1997; 97EP-0305215.
XX
XX (HUMA-) HUMAN GENOME SCI.
PA (SMK) SMITHKLINE BEECHAM PLC.
XX
PI Duckworth DM, Hastings GA, Ruben SM;
XX
DR WPI; 1999-083570/08.
DR N-PSDB; AAX18197.
XX

PT New human neurokinin B precursor (HPMBQ91) polypeptides and
PT polynucleotide - useful as diagnostic reagents and for prevention
PT and treatment of neuronal, metabolic, inflammatory and
PT gastrointestinal disorders, and cancers
XX

PS Claim 11; Page 14-15; 18pp; English.

XX This sequence is the human neurokinin B precursor HPMBQ91 of the
CC invention. HPMBQ91 polypeptides and polynucleotides are useful for
CC diagnosing susceptibility to diseases associated with HPMBQ91 protein
CC imbalance by determining HPMBQ91 polypeptide expression levels. HPMBQ91
CC polypeptides can be used to screen for agonists and antagonists by
CC measuring the binding to HPMBQ91, and observing the stimulation or
CC inhibition of HPMBQ91 function. These can be used in treatment to
CC activate or inhibit HPMBQ91 activity to treat conditions associated with
CC a lack of HPMBQ91 protein. Gene therapy may also be used to affect
CC endogenous HPMBQ91 polypeptide expression. HPMBQ91 antibodies are useful
CC for inducing an immune response to immunise and prevent disease, and for
CC isolating HPMBQ91 clones or purifying the polypeptides by affinity
CC chromatography. HPMBQ91 polypeptides can be administered directly or as a
CC vaccine to inoculate against disease. Diseases diagnosed, prevented and
CC treated include: neuronal disorders; CNS related disorders;
CC gastrointestinal and cardiovascular disorders; metabolic disorders
CC including diabetes and obesity; smooth muscle disorders; inflammatory
CC disorders; and cancers including adenomas, leiomyomas, liposarcomas,
CC melanomas, pulmonary chondroid hamartomas, lung, prostate and breast
CC cancer. The HPMBQ91 polypeptide is also useful for mapping the gene to a
CC chromosome, allowing gene inheritance to be studied through linkage
CC analysis, and tissue localisation studies, for determining HPMBQ91
XX expression patterns.

XX Sequence 121 AA;

Query Match 99.5%; Score 610; DB 20; Length 121;
Best Local Similarity 98.3%; Pred. No. 1.6e-65;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPQEEVPGGSRKRDPLYLQLLORLFKSHSLEGL 60
DB 1 mrimllftailafslaqsgavckepqeevpgggrskrdpdyqlqlgrfkshslegl 60
QY 61 LKALSOXSTDPKESTSPKRDHDFVFGXMGKRSVQPDSPDVGQENVPSCGILKYPBRA 120
DB 61 lkalsqastdpkestspkrdmhdfvfglmgrsvqpsdptdvnqenvpsfgilkyppra 120
QY 121 E 121
DB 121 e 121

RESULT 4

AA82380
ID AAB82380 standard; protein; 121 AA.

XX
AC AAB82380;

XX 23-JUL-2001 (first entry)

XX Human neurokinin B precursor.

XX

KW Neurokinin B; human; pregnancy; hypertension; pre-eclampsia;
KW diagnosis; therapy.

OS Homo sapiens.

FH Key Location/Qualifiers
FT Peptide 81..91
FT /label= Neurokinin

XX WO200136979-A2.

XX 25-MAY-2001.

XX 10-NOV-2000; 2000WO-GB04315.

XX 16-NOV-1999; 99GB-0027125.

XX (UTRE-) UNIV READING.

XX Page N, Lowry P;

XX WPI; 2001-355676/37.

XX N-PSDB; AAF90333, AAF90334.

XX Detecting production of the human precursor of neurokinin B by the
PT placenta in pregnancy induced hypertension or pre-eclampsia or related
PT foetal complication

XX Example 1; Fig 1; 63pp; English.

XX The present sequence is that of human neurokinin B (NKB) precursor.
CC The cloning of placental cDNA (see AAF90333) was used to identify
CC the NKB precursor. The precursor is processed to the 10-amino acid
CC NKB peptide. Detection of raised plasma levels of NKB, NKB
CC precursor, its breakdown product or variants at an early stage of
CC pregnancy provide an indication of the likely development of
CC pregnancy induced hypertension or pre-eclampsia. Reduction in the
CC levels of circulating NKB (or reduction of its effects) will
CC ameliorate the adverse effects upon the mother seen in these
CC conditions. Thus, the invention provides methods for predicting or
CC diagnosing pregnancy induced hypertension, pre-eclampsia or
CC related foetal complication based on measuring NKB levels in the
CC blood, and methods for preventing or treating these conditions,
CC e.g. by administering an agent that inhibits the biological
CC effect of NKB, such as an NK1, NK2 or NK3 antagonist.

XX Sequence 121 AA;

Query Match 99.5%; Score 610; DB 22; Length 121;
Best Local Similarity 98.3%; Pred. No. 1.6e-65;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEPQEEVPGGSRKRDPLYLQLLORLFKSHSLEGL 60
DB 1 mrimllftailafslaqsgavckepqeevpgggrskrdpdyqlqlgrfkshslegl 60
QY 61 LKALSOXSTDPKESTSPKRDHDFVFGXMGKRSVQPDSPDVGQENVPSCGILKYPBRA 120
DB 61 lkalsqastdpkestspkrdmhdfvfglmgrsvqpsdptdvnqenvpsfgilkyppra 120
QY 121 E 121
DB 121 e 121

RESULT 5

AAW75228

ID AAW75228 standard; Protein; 121 AA.

XX AAW75228;

XX 29-JAN-1999 (first entry)

DT

XX DE Human secreted protein encoded by gene 17 clone HPMBQ91.
 XX KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 67 /label= unknown
 FT Misc-difference 89 /label= unknown
 FT Misc-difference 89 /label= unknown
 XX PN W09840483-A2.
 XX PD 17-SEP-1998.
 XX PF 12-MAR-1998; 98WO-US04858.
 XX PR 19-DEC-1997; 97US-0068368.
 XX PR 14-MAR-1997; 97US-0040710.
 XX PR 14-MAR-1997; 97US-0040762.
 XX PR 30-MAY-1997; 97US-0048100.
 XX PR 30-MAY-1997; 97US-0048189.
 XX PR 30-MAY-1997; 97US-0048357.
 XX PR 30-MAY-1997; 97US-0050934.
 XX PR 06-JUN-1997; 97US-0048970.
 XX PR 05-SEP-1997; 97US-0057765.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Ferlie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;
 PI Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;
 PI Wei YF, Young PE, Zeng Z;
 XX DR WPI: 1998-520811/44.
 XX DR N-PSDB; AAV34318.
 XX PT Isolated human poly:nucleotide(s) encoding secretory peptide(s) -
 PT used to develop products for the diagnosis and treatment of e.g.
 PT inflammation, cancers, CNS disorders or immune system disorders
 XX PS Claim 1: Page 175; 201pp; English.
 XX CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. AAV34277) for increasing the stability of the fused
 CC protein as compared to the human protein only.
 CC The invention relates to 28 novel genes and their fragments (nucleic
 CC acid sequences: AAV34286-V34325; amino acid sequences AAV75196-W75235)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 28
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV34286 for described uses).
 XX Sequence 121 AA;

Query Match 99.3%; Score 609; DB 19; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.1e-65;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSFCAVCKEPOEEVVGGRSKRDPDLYQLLQRLFKSHSLEGL 60
 DB 1 mrmlmllftailafslagsfagvckepqeevvgggrskrdpdyqlqlrlfkahsslegl 60
 QY 61 LKALSOXSTDPRESTSPKRDMDHDFVGMGRSVQPDSPDVTNQENVPFGLKYPBRA 120
 DB 61 lkalsqstdpkstspkrdmdhdfvgmgrsvqpdspdvtnqenvpsfgilkyppra 120
 QY 121 E 121
 DB 121 e 121
 RESULT 6
 AAW96144
 ID AAW96144 standard; Protein; 122 AA.
 XX AC AAW96144;
 XX DT 27-APR-1999 (first entry)
 XX DE Human preprotachykinin B.
 XX KW Preprotachykinin B; PPT-B; neoplastic disorder;
 KW neurological disorder; Alzheimer's disease; amnesia;
 KW cerebral neoplasms; dementia; depression; Down's syndrome;
 KW Huntington's disease; multiple sclerosis; Parkinson's disease;
 KW paraneoplastic psychoses; schizophrenia; Tourette's disorder; angina;
 KW anaphylactic shock; asthma; cardiovascular shock;
 KW myocardial infarction; migraine.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 104 /label= Leu, Ser or Trp
 FT FT
 XX PN W09857986-A2.
 XX PD 23-DEC-1998.
 XX PF 19-JUN-1998; 98WO-US12855.
 XX PR 19-JUN-1997; 97US-0879995.
 XX PA (INCY-) INCYTE PHARM INC.
 XX PI Hillman JJ, Kaser MR, Lal P;
 XX DR WPI: 1999-080948/07.
 XX DR N-PSDB; AAX08906.
 XX PT New human preprotachykinin B - useful for treating neurological
 PT disorders and cancer
 XX PS Claim 1: Page 48-49; 57pp; English.
 XX CC Human preprotachykinin B (PPT-B) can be used to treat a
 CC neurological disorder. Antagonists of PPT-B can also be used in
 CC the treatment of neoplastic disorders. Particular neurological,
 CC disorders include akathisia, Alzheimer's disease, amnesia,
 CC amyotrophic lateral sclerosis, bipolar disorder, catatonia,
 CC cerebral neoplasms, dementia, depression, Down's syndrome, tardive
 CC dyskinesia, dystonias, Huntington's disease, multiple sclerosis,
 CC neurofibromatosis, Parkinson's disease, paranoid psychoses,
 CC schizophrenia, and Tourette's disorder. PPT-B or its agonist can
 CC also be used to treat angina, anaphylactic shock, arrhythmias,
 CC asthma, cardiovascular shock, Cushing's syndrome, hypertension,
 CC hypoglycemia, myocardial infarction, migraine and pheochromocytoma.
 XX Sequence 122 AA;

XX 05-APR-2000 (first entry)
XX Membrane-bound protein Prol155.
XX
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
XX Homo sapiens.
OS
XX
PN WO9963088-A2.
XX
PD 09-DEC-1999.
XX
XX 02-JUN-1999; 99WO-US12252.
XX 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 05-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 07-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096323.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.

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PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
DR WPI; 2000-072883/06.
DR N-PSDB; AAZ65085.
XX
PT Membrane-bound proteins and related nucleotide sequences
XX
PS claim 12; Fig 254; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
SQ Sequence . 135 AA;

Query Match 79.4%; Score 487; DB 21; Length 135;
Best Local Similarity 95.0%; Pred. No. 1.le-50;
Matches 96; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSFAGVCKPEQEEVPGGSRKRDPLYOLLQRLFKSHSLGL 60
Db 1 mrimllftailafslaqsfagvckpeqeevpggskrdpdyllqrlfkshsslegl 60

Qy 61 LKALSQXSTDPKSTSPKRDHDFVFGXMGKRSVQPSPT 101
Db 61 lkalsqstdpkstspkrdmhdffvlgmgkrsvqpegkt 101

RESULT 9
AAB65262
ID AAB65262 standard; Protein; 135 AA.
XX
AC AAB65262;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1155 (UNQ585) protein sequence SEQ ID NO:359.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.

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PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 02-MAR-2000; 2000WO-US05004.
PR 15-MAR-2000; 2000WO-US05841.
PR 20-MAR-2000; 2000WO-US06884.
XX
XX (GETH ) GENENTECH INC.
FA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrata N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
DR N-PSDB; AAF44231.
XX
PT PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
XX
XX Claim 12; Fig 254; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 135 AA;

Query Match 79.4%; Score 487; DB 22; Length 135;
Best Local Similarity 95.0%; Pred. No. 1.le-50;
Matches 96; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MRIMLLFTAILAFSLAQSFAGVCKPEQEEVPGGSRKRDPLYOLLQRLFKSHSLGL 60
Db 1 mrimllftailafslaqsfagvckpeqeevpggskrdpdyllqrlfkshsslegl 60

Qy 61 LKALSQXSTDPKSTSPKRDHDFVFGXMGKRSVQPSPT 101
Db 61 lkalsqstdpkstspkrdmhdffvlgmgkrsvqpegkt 101

RESULT 10

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AAW96145
ID AAW96145 standard; Protein; 126 AA.

XX
AC AAW96145;

XX
DT 27-APR-1999 (first entry)

XX
DE Bovine preprotachykinin B.

XX
KW Preprotachykinin B; PPT-B; neoplastic disorder;
KW neurological disorder; Alzheimer's disease; amnesia;
KW cerebral neoplasms; dementia; depression; Down's syndrome;
KW Huntington's disease; multiple sclerosis; Parkinson's disease;
KW paranoid psychoses; schizophrenia; Tourette's disorder; angina;
KW anaphylactic shock; asthma; cardiovascular shock;
KW myocardial infarction; migraine.

XX
OS Bos taurus.

XX
PN WO9857986-A2.

XX
PD 23-DEC-1998.

XX
PF 19-JUN-1998; 98WO-US12855.

XX
PR 19-JUN-1997; 97US-0879995.

XX
PA (INCY-) INCYTE PHARM INC.

XX
PI Hillman JJ, Kaser MR, Lal P;

XX
XX WPI; 1999-080948/07.

XX
PT New human preprotachykinin B - useful for treating neurological
PT disorders and cancer

XX
PS Disclosure; Figure 2; 57pp; English.

XX
CC Human preprotachykinin B (AAW96144) (PPT-B) can be used to treat a
CC neurological disorder. Antagonists of PPT-B can also be used in
CC the treatment of neoplastic disorders. Particular neurological,
CC disorders include akathisia, Alzheimer's disease, amnesia,
CC amyotrophic lateral sclerosis, bipolar disorder, catatonia,
CC cerebral neoplasms, dementia, depression, Down's syndrome, tardive
CC dyskinesia, dystonias, Huntington's disease, multiple sclerosis,
CC neurofibromatosis, Parkinson's disease, paranoid psychoses,
CC schizophrenia, and Tourette's disorder. PPT-B or its agonist can
CC also be used to treat angina, anaphylactic shock, arrhythmias,
CC asthma, cardiovascular shock, Cushing's syndrome, hypertension,
CC hypoglycemia, myocardial infarction, migraine and pheochromocytoma.

XX
SQ Sequence 126 AA;

Query Match 66.5%; Score 407.5; DB 20; Length 126;
Best Local Similarity 64.3%; Pred. No. 3.7e-41;
Matches 81; Conservative 15; Mismatches 25; Indels 5; Gaps 2;

QY 1 MRIMLFTAILAFSAQSGAVCKEPOEEVPGGSKRDPDLYQ----LLQRLFKSH-S 55
DB 1 mrstllfavlalsarslgavceeseqvpggghskdsnlqldppslrrlydsrvv 60
QY 56 SLEGLLKALQSQTDPKSTSPKRDMDHFFVCGXMGKRSVQDPSPTDVNOENVPSFGILK 115
DB 61 sidgllkmlskasvpgkpslpqkrdmhdfvglmgrknlpdpvdingenipsfgtfk 120

QY 116 YPPRAE 121

DB 121 yppsve 126

RESULT 11
AAW96146

ID AAW96146 standard; Protein; 116 AA.

XX
AC AAW96146;

XX
DT 27-APR-1999 (first entry)

XX
DE Rat preprotachykinin B.

XX
KW Preprotachykinin B; PPT-B; neoplastic disorder;
KW neurological disorder; Alzheimer's disease; amnesia;
KW cerebral neoplasms; dementia; depression; Down's syndrome;
KW Huntington's disease; multiple sclerosis; Parkinson's disease;
KW paranoid psychoses; schizophrenia; Tourette's disorder; angina;
KW anaphylactic shock; asthma; cardiovascular shock;
KW myocardial infarction; migraine.

XX
OS Rattus rattus.

XX
PN WO9857986-A2.

XX
PD 23-DEC-1998.

XX
PF 19-JUN-1998; 98WO-US12855.

XX
PR 19-JUN-1997; 97US-0879995.

XX
PA (INCY-) INCYTE PHARM INC.

XX
PI Hillman JJ, Kaser MR, Lal P;

XX
XX WPI; 1999-080948/07.

XX
PT New human preprotachykinin B - useful for treating neurological
PT disorders and cancer

XX
PS Disclosure; Figure 2; 57pp; English.

XX
CC Human preprotachykinin B (AAW96144) (PPT-B) can be used to treat a
CC neurological disorder. Antagonists of PPT-B can also be used in
CC the treatment of neoplastic disorders. Particular neurological,
CC disorders include akathisia, Alzheimer's disease, amnesia,
CC amyotrophic lateral sclerosis, bipolar disorder, catatonia,
CC cerebral neoplasms, dementia, depression, Down's syndrome, tardive
CC dyskinesia, dystonias, Huntington's disease, multiple sclerosis,
CC neurofibromatosis, Parkinson's disease, paranoid psychoses,
CC schizophrenia, and Tourette's disorder. PPT-B or its agonist can
CC also be used to treat angina, anaphylactic shock, arrhythmias,
CC asthma, cardiovascular shock, Cushing's syndrome, hypertension,
CC hypoglycemia, myocardial infarction, migraine and pheochromocytoma.

XX
SQ Sequence 116 AA;

Query Match 56.2%; Score 344.5; DB 20; Length 116;
Best Local Similarity 60.0%; Pred. No. 1.3e-33;
Matches 72; Conservative 16; Mismatches 23; Indels 9; Gaps 3;

QY 1 MRIMLFTAILAFSAQSGAVCKEPOEEVPGGSKRDPDLY-----QLQRLFKSHS- 55
DB 1 mrsamlaaavalslawtfgaaceeqeq---ggrlskdsdlslppllrrlydsrsi 56
QY 56 SLEGLLKALQSQTDPKSTSPKRDMDHFFVCGXMGKRSVQDPSPTDVNOENVPSFGILK 115
DB 57 siegllkvlksasvpgkpslpqkrdmhdfvglmgrknsqdpadvveentpsfgvik 116

RESULT 12
AAW97214

ID AAW97214 standard; Protein; 92 AA.

XX
AC AAW97214;

XX
DT 07-MAY-1999 (first entry)

KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX Homo sapiens.

OS
 PN W09840483-A2.

XX
 PD 17-SEP-1998.

XX
 PF 12-MAR-1998; 98WO-US04858.

XX
 PR 19-DEC-1997; 97US-0068368.

XX
 PR 14-MAR-1997; 97US-0040710.

XX
 PR 30-MAY-1997; 97US-0040762.

XX
 PR 30-MAY-1997; 97US-0048100.

XX
 PR 30-MAY-1997; 97US-0048189.

XX
 PR 30-MAY-1997; 97US-0048357.

XX
 PR 06-JUN-1997; 97US-0050934.

XX
 PR 05-SEP-1997; 97US-0048970.

XX
 PR 05-SEP-1997; 97US-0057765.

XX
 PA (HUMA-) HUMAN GENOME SCI INC.

XX
 PI Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;

XX
 PI Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;

XX
 PI Wei YF, Young PE, Zeng Z;

XX
 DR N-PSDB; AAV34302.

XX
 DR WPI: 1998-520811/44.

XX
 DR N-PSDB; AAV34302.

XX
 PT Isolated human poly:nucleotide(s) encoding secretory peptide(s) -

XX
 PT used to develop products for the diagnosis and treatment of e.g.

XX
 PT inflammation, cancers, CNS disorders or immune system disorders

XX
 XX Disclosure; Page 19; 20lpp; English.

XX
 PS This sequence represents a fragment of a secreted human protein encoded

XX
 CC by the nucleic acid molecule designated Gene 17 (AAV34302). The gene

XX
 CC can be used to generate fusion proteins by linking to the gene to a

XX
 CC human immunoglobulin Fc portion (e.g. AAV34277) for increasing the

XX
 CC stability of the fused protein as compared to the human protein only.

XX
 CC The invention relates to 28 novel genes and their fragments (nucleic

XX
 CC acid sequences: AAV34286-V34325; amino acid sequences AAV75196-W75235)

XX
 CC which are useful for preventing, treating or ameliorating medical

XX
 CC conditions e.g. by protein or gene therapy. Also, pathological

XX
 CC conditions can be diagnosed by determining the amount of the new

XX
 CC polypeptides in a sample or by determining the presence of mutations in

XX
 CC the new polynucleotides. Specific uses are described for each of the 28

XX
 CC polynucleotides, based on which tissues they are most highly expressed in

XX
 CC (see AAV34286 for described uses).

XX
 CC Sequence 36 AA;

XX
 SQ

Query Match 31.0%; Score 190; DB 19; Length 36;
 Best Local Similarity 97.2%; Pred. No. 1e-15;
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 77 PEKRDHDFVGVGMKRSVQPSPTDVENVPSPG 112
 Db 1 pekrdmhdfvglmgrsvqpsptdvnqenvpsfg 36
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 |||||

RESULT 15
 AAW74414
 ID AAW74414 standard; Protein; 39 AA.
 XX
 AC AAW74414;
 XX
 DT 10-MAY-1999 (first entry)
 XX

Search completed: May 3, 2002, 12:24:06
 Job time: 203 sec

HPMBQ91 protein sequence fragment.
 HPMBQ91; neurokinin B precursor; neuronal disorder; CNS related disorder;
 gastrointestinal disorder; cardiovascular disorder; metabolic disorder;
 smooth muscle disorder; inflammatory disorder; cancer; gene therapy.
 Homo sapiens.
 EP892053-A2.
 20-JAN-1999.
 26-JUN-1998; 98EP-0305066.
 14-JUL-1997; 97EP-0305215.
 (HUMA-) HUMAN GENOME SCI.
 (SMIK) SMITHKLINE BEECHAM PLC.
 Duckworth DM, Hastings GA, Ruben SM;
 WPI: 1999-083570/08.
 New human neurokinin B precursor (HPMBQ91) polypeptides and
 polynucleotide - useful as diagnostic reagents and for prevention
 and treatment of neuronal, metabolic, inflammatory and
 gastrointestinal disorders, and cancers
 Claim 14; Page 15; 18pp; English.
 This sequence is the human neurokinin B precursor HPMBQ91 of the
 invention. HPMBQ91 polypeptides and polynucleotides are useful for
 diagnosing susceptibility to diseases associated with HPMBQ91 protein
 imbalance by determining HPMBQ91 polypeptide expression levels. HPMBQ91
 polypeptides can be used to screen for agonists and antagonists by
 measuring the binding to HPMBQ91, and observing the stimulation or
 inhibition of HPMBQ91 function. These can be used in treatment or
 activate or inhibit HPMBQ91 activity to treat conditions associated with
 a lack of HPMBQ91 protein. Gene therapy may also be used to affect
 endogenous HPMBQ91 polypeptide expression. HPMBQ91 antibodies are useful
 for inducing an immune response to immunise and prevent disease, and for
 isolating HPMBQ91 clones or purifying the polypeptides by affinity
 chromatography. HPMBQ91 polypeptides can be administered directly or as a
 vaccine to inoculate against disease. Diseases diagnosed, prevented and
 treated include: neuronal disorders; CNS related disorders;
 gastrointestinal and cardiovascular disorders; metabolic disorders;
 including diabetes and obesity; smooth muscle disorders; inflammatory
 disorders; and cancers including adenomas, leiomyomas, liposarcomas,
 melanomas, pulmonary chondroid hamartomas, lung, prostate and breast
 cancer. The HPMBQ91 polypeptide is also useful for mapping the gene to a
 chromosome, allowing gene inheritance to be studied through linkage
 analysis, and tissue localisation studies, for determining HPMBQ91
 expression patterns.

Query Match 31.0%; Score 190; DB 20; Length 39;
 Best Local Similarity 97.4%; Pred. No. 1.1e-15;
 Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 40 DPDIYQLLQRLFKSHSLEGLLKALSOXSTDPEKSTSP 78
 Db 1 dpdiylqlrlfkshsslegllkalsqstdpkestpspe 39
 |||||
 |||||

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 12:22:33 ; Search time 12.48 Seconds
(without alignments)
218.181 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 613
Sequence: 1 MRMLFTALFSLAQSG.....DVNQENVSPGILKYPRAE 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.AA.*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	592.5	96.7	122	2	US-08-879-995A-1
2	592.5	96.7	122	3	US-09-215-096-1
3	407.5	66.5	126	2	US-08-879-995A-3
4	407.5	66.5	126	3	US-09-215-096-3
5	344.5	56.2	116	2	US-08-879-995A-4
6	344.5	56.2	116	3	US-09-215-096-4
7	69	11.3	863	2	US-08-380-182-19
8	69	11.3	863	3	US-08-380-182-20
9	67.5	11.0	382	2	US-08-582-740-70
10	67.5	11.0	382	4	US-09-109-879-70
11	64.5	10.5	647	2	US-08-770-761A-8
12	64.5	10.5	705	2	US-08-770-761A-7
13	64.5	10.5	1005	2	US-08-935-450-2
14	64	10.4	130	6	5268359-2
15	64	10.4	284	1	US-08-390-858B-36
16	63	10.3	444	3	US-09-221-235-14
17	63	10.3	444	3	US-09-221-928-14
18	63	10.3	444	4	US-09-221-527-14
19	63	10.3	444	4	US-09-221-236-14
20	63	10.3	444	4	US-09-221-416-14
21	63	10.3	444	4	US-09-221-245-14
22	63	10.3	444	4	US-09-163-115-14
23	63	10.3	444	4	US-09-221-528-14
24	63	10.3	444	4	US-09-593-553-14
25	63	10.3	444	4	US-09-221-237-14
26	63	10.3	1360	4	US-09-393-569-2
27	63	10.3	1503	4	US-08-976-255-14

28	61.5	10.0	618	2	US-08-770-761A-3	Sequence 3, Appli
29	61.5	10.0	660	2	US-08-770-761A-2	Sequence 2, Appli
30	61.5	10.0	662	2	US-08-770-761A-5	Sequence 5, Appli
31	61.5	10.0	3118	2	US-08-457-273B-8	Sequence 8, Appli
32	61.5	10.0	3119	1	US-08-246-982A-16	Sequence 16, Appli
33	61.5	10.0	3119	1	US-08-453-265-16	Sequence 16, Appli
34	61.5	10.0	3144	1	US-08-246-982A-6	Sequence 6, Appli
35	61.5	10.0	3144	1	US-08-453-265-6	Sequence 6, Appli
36	61.5	10.0	3144	2	US-08-457-273B-42	Sequence 42, Appli
37	61.5	10.0	3144	3	US-08-556-419-21	Sequence 21, Appli
38	61.5	10.0	3144	4	US-09-041-886-15	Sequence 15, Appli
39	61	10.0	205	3	US-08-989-251-27	Sequence 27, Appli
40	61	10.0	205	3	US-08-989-251-37	Sequence 37, Appli
41	61	10.0	205	3	US-09-340-250-27	Sequence 27, Appli
42	61	10.0	205	3	US-09-340-250-37	Sequence 37, Appli
43	61	10.0	348	2	US-08-953-041-2	Sequence 2, Appli
44	61	10.0	348	4	US-09-159-417-2	Sequence 2, Appli
45	61	10.0	874	2	US-08-456-647B-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-879-995A-1
; Sequence 1, Application US/08879995A
; Patent No. 5985606
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/879,995A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT03
; CLONE: 2109906
; US-08-879-995A-1

Query Match 96.7%; Score 592.5; DB 2; Length 122;

Best Local Similarity 95.9%; Pred. No. 4.6e-66;
Matches 117; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEQQEVEVPGGGRKRDPLDYQLLQRLFKSHSSLEGL 60
||||| MRIMLLFTAILAFSLAQSGAVCKEQQEVEVPGGGRKRDPLDYQLLQRLFKSHSSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSGAVCKEQQEVEVPGGGRKRDPLDYQLLQRLFKSHSSLEGL 60
QY 61 LKALSQSTDPKSTSPKRDMDHFFVGLMGKRSVQDPSPTDV-NOENVPSFGILKYPPR 119
||||| LKALSQSTDPKSTSPKRDMDHFFVGLMGKRSVQDPSPTDV-NOENVPSFGILKYPPR 119
Db 61 LKALSQSTDPKSTSPKRDMDHFFVGLMGKRSVQDPSPTDV-NOENVPSFGILKYPPR 120
QY 120 AE 121
||
Db 121 AE 122

RESULT 2

US-09-215-096-1
; Sequence 1, Application US/09215096
; Patent No. 6008194
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT03
; CLONE: 2109906
US-09-215-096-1

Query Match 96.7%; Score 592.5; DB 3; Length 122;
Best Local Similarity 95.9%; Pred. No. 4.6e-66;
Matches 117; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEQQEVEVPGGGRKRDPLDYQLLQRLFKSHSSLEGL 60
||||| MRIMLLFTAILAFSLAQSGAVCKEQQEVEVPGGGRKRDPLDYQLLQRLFKSHSSLEGL 60
Db 1 MRIMLLFTAILAFSLAQSGAVCKEQQEVEVPGGGRKRDPLDYQLLQRLFKSHSSLEGL 60

QY 61 LKALSQSTDPKSTSPKRDMDHFFVGLMGKRSVQDPSPTDV-NOENVPSFGILKYPPR 119
||||| LKALSQSTDPKSTSPKRDMDHFFVGLMGKRSVQDPSPTDV-NOENVPSFGILKYPPR 119
Db 61 LKALSQSTDPKSTSPKRDMDHFFVGLMGKRSVQDPSPTDV-NOENVPSFGILKYPPR 120
QY 120 AE 121
||
Db 121 AE 122

RESULT 3

US-08-879-995A-3
; Sequence 3, Application US/08879995A
; Patent No. 5985606
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/879,995A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 163590
US-08-879-995A-3

Query Match 66.5%; Score 407.5; DB 2; Length 126;
Best Local Similarity 64.3%; Pred. No. 4.3e-43;
Matches 81; Conservative 15; Mismatches 25; Indels 5; Gaps 2;

QY 1 MRIMLLFTAILAFSLAQSGAVCKEQQEVEVPGGGRKRDPLDYQLLQRLFKSHSSLEGL 119
||||| MRIMLLFTAILAFSLAQSGAVCKEQQEVEVPGGGRKRDPLDYQLLQRLFKSHSSLEGL 119
Db 1 MRIMLLFTAILAFSLAQSGAVCKEQQEVEVPGGGRKRDPLDYQLLQRLFKSHSSLEGL 120
QY 56 SLEGLLKALSOXSTDPKSTSPKRDMDHFFVGLMGKRSVQDPSPTDV-NOENVPSFGILKYPPR 115
||||| SLEGLLKALSOXSTDPKSTSPKRDMDHFFVGLMGKRSVQDPSPTDV-NOENVPSFGILKYPPR 115
Db 61 SLDGGLKMLSKASVGVKPSLPQKRDMDHFFVGLMGKRSVQDPSPTDV-NOENVPSFGILKYPPR 120
QY 116 YPPRAE 121
||
Db 121 YPPSVE 126

RESULT 4
US-09-215-096-3
; Sequence 3, Application US/09215096
; Patent No. 6008194
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215.096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 163590
US-09-215-096-3

Query Match 66.5%; Score 407.5; DB 3; Length 126;
Best Local Similarity 64.3%; Pred. No. 4.3e-43;
Matches 81; Conservative 15; Mismatches 25; Indels 5; Gaps 2;
Qy 1 MRIMLLFTAILAFSLAQSGAVCKEPOEVVPGGSRKRDPLYQ-----LLQRLFKSH-S 55
Db 1 MRSTLLFAVILALSSARSILGAVCEESQEVVPGGSHKSDSNLYQLPPSLLRLLYDSRVV 60
Qy 56 SLEGLLKALSOXSTDPKSTSPKEDMHDFFVGMKRSVQDPDPTDYNQENVPSPFGILK 115
Db 61 SLDGLLKLMSKASVGPKEPQKRDMDHFFVGLMGKRNLPQDPTDVPDINQENIPSGFTFK 120
Qy 116 YPPRAE 121
Db 121 YPPSVE 126

RESULT 5
US-08-879-995A-4
; Sequence 4, Application US/08879995A
; Patent No. 5985606
; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/879,995A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 205725
US-08-879-995A-4

Query Match 56.2%; Score 344.5; DB 2; Length 116;
Best Local Similarity 60.0%; Pred. No. 2.5e-35;
Matches 72; Conservative 16; Mismatches 23; Indels 9; Gaps 3;

Qy 1 MRIMLLFTAILAFSLAQSGAVCKEPOEVVPGGSRKRDPLY-----OLLQRLFKSHS- 55
Db 1 MRSAMLFVAVLALSLAWTFGAACEEPEQ-----GGRLSKDSDLPLPPPLRLLYDSRSI 56
Qy 56 SLEGLLKALSOXSTDPKSTSPKEDMHDFFVGMKRSVQDPDPTDYNQENVPSPFGILK 115
Db 57 SLEGLLKLMSKASVGPKEPQKRDMDHFFVGLMGKRNQSDPTDADVVEENTPSPGVILK 116

RESULT 6
US-09-215-096-4
; Sequence 4, Application US/09215096
; Patent No. 6008194
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA

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; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/215,096
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 205725
; US-09-215-096--4

Query Match 56.2%; Score 344.5; DB 3; Length 116;
Best Local Similarity 60.0%; Pred. No. 2.5e-35;
Matches 72; Conservative 16; Mismatches 23; Indels 9; Gaps 3;

QY 1 MRIMLFTALAFSLAQSGAVCKEPEVEYVPGGRSKRDPDLY----QLQLRLFKSHS- 55
   || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 1 MRSAMLFVAVALSLAWTFCAACEPEEQ-----GGRLSKDSLSLLPPPLLRLLYSRSI 56

QY 56 SLEGLLKALSOXTDTPKSTSPKRDHDFVCGXMKRSVPQPSPTDVNQENVPSFGILK 115
||||| || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 57 SLEGLLVKSASVGPKETSLPQKRDMHDFVGLMGKRNQPDPADVVBEPTPFSGVLK 116

RESULT 7
US-08-380-182-19
; Sequence 19, Application US/08380182
; Patent No. 5858749
; GENERAL INFORMATION:
; APPLICANT: Matthews, Benjamin F.
; TITLE OF INVENTION: A Bifunctional Protein From Carrots
; TITLE OF INVENTION: (Daucus carota) with Aspartokinase and Homoserine
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janelle S. Graeter
; STREET: Room 411,Bldg. 005, BARC-W
; CITY: Beltsville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20705
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/380,182
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Graeter, Janelle S.
; REGISTRATION NUMBER: 35,024
; REFERENCE/DOCKET NUMBER: 0226.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-504-6629
; TELEFAX: 301-504-5060
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 863 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Daucus carota

; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/215,096
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Graeter, Janelle S.
; REGISTRATION NUMBER: 35,024
; REFERENCE/DOCKET NUMBER: 0226.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-504-6629
; TELEFAX: 301-504-5060
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 863 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Daucus carota

; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/215,096
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Graeter, Janelle S.
; REGISTRATION NUMBER: 35,024
; REFERENCE/DOCKET NUMBER: 0226.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-504-6629
; TELEFAX: 301-504-5060
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 863 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Daucus carota

; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/215,096
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Graeter, Janelle S.
; REGISTRATION NUMBER: 35,024
; REFERENCE/DOCKET NUMBER: 0226.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-504-6629
; TELEFAX: 301-504-5060
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 863 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Daucus carota

; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
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; REGISTRATION NUMBER: 35,024
; REFERENCE/DOCKET NUMBER: 0226.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-504-6629
; TELEFAX: 301-504-5060
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 863 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Daucus carota

; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
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; TELECOMMUNICATION INFORMATION:
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; TELEFAX: 301-504-5060
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 863 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Daucus carota

; ZIP: 94304
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; FILING DATE:
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; TELEFAX: 301-504-5060
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; SEQUENCE CHARACTERISTICS:
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Daucus carota

; ZIP: 94304
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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
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; APPLICATION NUMBER: US/09/215,096
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
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; REGISTRATION NUMBER: 35,024
; REFERENCE/DOCKET NUMBER: 0226.94
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; TELEFAX: 301-504-5060
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; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Daucus carota

; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Graeter, Janelle S.
; REGISTRATION NUMBER: 35,024
; REFERENCE/DOCKET NUMBER: 0226.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-504-6629
; TELEFAX: 301-504-5060
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 863 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Daucus carota

; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/215,096
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Graeter, Janelle S.
; REGISTRATION NUMBER: 35,024
; REFERENCE/DOCKET NUMBER: 0226.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-504-6629
; TELEFAX: 301-504-5060
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 863 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Daucus carota

; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/215,096
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Graeter, Janelle S.
;
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US-08-380-182-20

Query Match 11.3%; Score 69; DB 2; Length 863;
Best Local Similarity 31.2%; Pred. No. 6.1;
Matches 29; Conservative 12; Mismatches 42; Indels 10; Gaps 3;
Qy 30 VYPGGGRKPDYQLQRLFKSHSSLE-GLLKALSOXSTDPKSTSPKRDMDHDFVVG 88
Db 185 VYNPAGSNQVDYDYLESEKRLKWFSSQOCOTIVATGFIATPQNIPTTLKRDGSDFSAA 244
Qy 89 XMKG--RSVQPSDPTDVNQENVPSEGIILKYP 119
Db 245 IMGALLRAGQVTIWDVN-----GVYSADPR 270

RESULT 9
US-08-582-740-70
; Sequence 70, Application US/08582740
; Patent No. 6037324
; GENERAL INFORMATION:
; APPLICANT: Schwender, Charles F.
; APPLICANT: Shroff, Hitesh N.
; TITLE OF INVENTION: Inhibitors of MacCAM-1-Mediated
; TITLE OF INVENTION: Interactions and Methods of Use Therefor
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/582,740
; FILING DATE: 04-JAN-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-12
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-582-740-70

Query Match 11.0%; Score 67.5; DB 3; Length 382;
Best Local Similarity 25.4%; Pred. No. 3;
Matches 33; Conservative 15; Mismatches 27; Indels 55; Gaps 7;
Qy 11 LAFSL-----AQSFGAVCKEPQEEVPGGSRKRPD-LYQLLOR----- 49
Db 147 LSFSLVGGQLEGAALGPVEVEEE--PQG-----DEDVLFRTWRRLPLGTPVP 199
Qy 50 -----LFKSHSSLEGLLKALSOXSTDPKSTSPKRDMDHDFVVGXMKGRSVQ 96
Db 200 PALYCOATMRPLGELSHRQAIPVLH--SPTSPEPDTTSPSPD-----TTS 245
Qy 97 PDSPTDVNOE 106
Db 246 PESPDTSQE 255

RESULT 10
US-09-109-879-70
; Sequence 70, Application US/09109879
; Patent No. 6274556
; GENERAL INFORMATION:
; APPLICANT: Schwender, Charles F.
; APPLICANT: Shroff, Hitesh N.
; TITLE OF INVENTION: INHIBITORS OF MACCAM-1-MEDIATED
; TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02421
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/109,879
; FILING DATE: 02-JUL-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00291
; FILING DATE: 03-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/582,740
; FILING DATE: 04-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-12A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-109-879-70

Query Match 11.0%; Score 67.5; DB 4; Length 382;
Best Local Similarity 25.4%; Pred. No. 3;
Matches 33; Conservative 15; Mismatches 27; Indels 55; Gaps 7;
Qy 11 LAFSL-----AQSFGAVCKEPQEEVPGGSRKRPD-LYQLLOR----- 49
Db 147 LSFSLVGGQLEGAALGPVEVEEE--PQG-----DEDVLFRTWRRLPLGTPVP 199
Qy 50 -----LFKSHSSLEGLLKALSOXSTDPKSTSPKRDMDHDFVVGXMKGRSVQ 96
Db 200 PALYCOATMRPLGELSHRQAIPVLH--SPTSPEPDTTSPSPD-----TTS 245
Qy 97 PDSPTDVNOE 106
Db 246 PESPDTSQE 255

RESULT 11
US-08-770-761A-8
; Sequence 8, Application US/08770761A
; Patent No. 5814503
; GENERAL INFORMATION:
; APPLICANT: Kovacevic, Steven

GENERAL INFORMATION:
APPLICANT: Kovacevic, Steven
APPLICANT: Otto, Keith A.
APPLICANT: Rao, Ramachandra N.
TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
TITLE OF INVENTION: REGULATORY PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: IN
COUNTRY: USA
ZIP: 46285

```

Query Match      10.5%; Score 64.5; DB 2; Length 1005;
Best Local Similarity 23.9%; Pred. No. 27;
Matches 28; Conservative 13; Mismatches 57; Indels 19; Gaps 3;

      QY      6 LFTAILAFSLAQSGAYCKPQPEVPGGKRSKRPDLQYLQRLFKSHSLLEGLLKALS 65
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      Ddb      297 LFPQSGASVPQSGNALGDVDDGEVPLREKEKK-----VRPE-----SMFDAVD 341
      QY      66 QXSTDPKRESTSPKRRMDHFEF---VGXMGKRSVQDPDSTDVNQENVPFSGILKYPP 118

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US-08-390-858B-36

Query Match      10.4%; Score 64; DB 1; Length 284;
Best Local Similarity 29.1%; Pred. No. 5.4;
Matches 25; Conservative 14; Mismatches 31; Indels 16; Gaps

QY 32 PGGGRSRDPDLVQLLORLFKSHSLEGLL----KALSOXSTDPKESTPEKRDMDHFFV 87
   | ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 103 PNTGSRSGFGFI-----LPFKAASVEKVLDQKEHRLDGRVIDPKAMANKDPVKKFV 156

QY 88 GXMGKRSVQPDSPDTVN-QENVPSFG 112
   | : |||| : |||
Db 157 G-----GLNPESPTTEEKIREYFGGEF 177

Search completed: May 3, 2002, 12:24:25
Job time: 112 sec
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RESULT 15
US-08-390-858B-36
; Sequence 36, Application US/08390858B
; Patent No. 5643727
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Harigai, Masayoshi
; TITLE OF INVENTION: Bcl-2 Gene Inhibitory Element Binding
; TITLE OF INVENTION: Factor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390, 858B
; FILING DATE: 16-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1366
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 284 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	407.5	66.5	126	2	A25905	tachykinin B precursor
2	364.5	59.5	116	2	I65342	tachykinin B precursor
3	344.5	56.2	116	2	A43779	neurokinin B precursor
4	78.5	12.6	2380	2	T29551	hypothetical protein
5	77	12.8	1008	2	T05578	hypothetical protein
6	77	12.6	2211	1	KPB05	coagulation factor
7	72.5	11.8	1711	2	T21432	hypothetical protein
8	70	11.4	969	2	A75634	MCB-related protein
9	69.5	11.3	437	2	T26767	hypothetical protein
10	69	11.3	921	2	S35160	hypothetical protein
11	68.5	11.2	1126	2	JC4019	aspartate kinase (
12	68	11.1	293	1	B44502	DNA mismatch repair
13	68	11.1	452	2	S73266	nonstructural protein
14	68	11.1	808	2	G65185	translation initiation
15	68	11.1	906	2	T47340	hypothetical protein
16	67.5	11.0	578	2	T48795	hypothetical protein
17	67.5	11.0	978	1	RGBY13	origin recognition
18	67	10.9	823	2	T16758	regulatory protein
19	66.5	10.8	929	2	A32495	hypothetical protein
20	66	10.8	211	2	A42261	rep-1 protein, for
21	66	10.8	343	2	S34811	heparan sulfate prote
22	66	10.8	848	2	A33810	mating factor Mar1
23	65.5	10.7	839	2	A25908	band 3 anion trans
24	65.5	10.7	911	1	B3HU	hypothetical protein
25	65.5	10.7	1880	2	T18531	band 3 anion trans
26	65	10.6	282	2	S46793	tractin - mediana
27	65	10.6	343	2	S66173	vacuolar protein s
28	65	10.6	742	2	D86160	mating factor Mar-
29	65	10.6	793	2	T31655	hypothetical protein
30	65	10.6	793	2	T31655	DNA excision repair

A; Residues: 1-116 <N

Biomed. Res. 14, 253-259, 1993

A: Pathway: blood coagulation
C: Superfamily: coagulation factor V; discolidin I amino-terminal homology; ferroxidase re
C: Keywords: blood coagulation; duplication; glycoprotein; phospholipid binding; plasma;
F: 1-26/Domain: signal sequence #status predicted <SIG>
F: 29-2211/Product: coagulation factor V #status predicted <MAT>
F: 29-741/Product: coagulation factor Va heavy chain #status predicted <VAL>
F: 29-345/Domain: A1 <DAL>
F: 33-329/Domain: ferroxidase repeat homology <FOI>
F: 346-695/Domain: A2 <DA2>
F: 351-688/Domain: ferroxidase repeat homology <FO2>
F: 696-1564/Domain: B <DOB>
F: 1175-1437/Region: 9-residue repeats (Q-X-T-N-L-S-P-D-L-S)
F: 1565-2211/Product: coagulation factor Va light chain #status predicted <VAL>
F: 1565-1892/Domain: A3 <DA3>
F: 1572-1892/Domain: ferroxidase repeat homology <FO3>
F: 1654-1752/Region: phospholipid binding #status predicted
F: 1893-2051/Domain: C1 <DC1>
F: 1893-2048/Domain: discolidin I amino-terminal homology <DN1>
F: 2052-2211/Domain: C2 <DC2>
F: 2052-2208/Domain: discolidin I amino-terminal homology <DN2>
F: 167-193-248-329-499-525/Disulfide bonds: #status experimental
F: 225-239-297-382-460-553-587-745-756-774-780-902-952-964-1044-1053-1062-1071-1078-1094-
F: 334-335/Cleavage site: Arg-Asn (protein C) #status predicted
F: 363-697/Binding site: sulfate (Tyr) (covalent) #status predicted
F: 376-377/Cleavage site: Arg-Ser (coagulation factor Xa) #status predicted
F: 533-534/Cleavage site: Arg-Gly (protein C) #status predicted
F: 607-688-1712-1738-1894-2048-2053-2208/Disulfide bonds: #status predicted
F: 741-742/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status predicted
F: 1034-1035/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status predicted
F: 1564-1565/Cleavage site: Arg-Ser (thrombin) #status experimental

Query Match 12.6%; Score 77; DB 1; Length 2211;
Best Local Similarity 28.6%; Pred. No. 24;
Matches 33; Conservative 13; Mismatches 39; Indels 28; Gaps 6;

QY 14 SLAOSFGAVCKEP---QEYVPGGGRKRPDLYQ-----LQRLFKSHSSLEGLKAL 64
DB 1269 SLSPDLGOTALSPDPGQESLSPDLGQTSLSQESLSPDLGQTSLSPPQESLSPDL 1328
QY 65 SQXSTDP---KESLSPKRDHDFVFXGCKRSVQDPSPDYNQENV-PSFG 112
DB 1329 GOTALSPDPGQESLSPD-----LGQTSLSP-----DLQESLSPDLG 1365

RESULT 7
T21432
hypothetical protein F26H11.2 - Caenorhabditis elegans
C: Species: Caenorhabditis elegans
C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C: Accession: T21432
R: Barlow, K.
submitted to the EMBL Data Library, November 1996
A: Reference number: Z19421
A: Accession: T21432
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-1711 <WIL>
A: Cross-references: EMBL:Z81515; PIDN: CAB04197.1; GSPDB: GN00020; CESP: F26H11.2
A: Experimental source: clone F26H11
C: Genetics:
A: Gene: CESP: F26H11.2
A: Map position: 2
A: Introns: 56/3; 154/2; 373/2; 417/3; 505/2; 596/1; 703/2; 847/3; 922/3; 1034/2; 1078/2;

Query Match 11.8%; Score 72.5; DB 2; Length 1711;
Best Local Similarity 25.6%; Pred. No. 52;
Matches 30; Conservative 16; Mismatches 44; Indels 27; Gaps 5;

QY 4 MLLFTAILAFS---LAOSFGAVCKEPQEYVPGGGRKRPDLYQLLQRLFKSHSSLEGL 60
DB 28 LMVFLIMLYSDCHFSQILLIFLQRPYDMDAPPGRSKR-----KHPSESG- 73

QY 61 LKALSOXSTDPKESTSPE-----KRDHMD-FFVFXGCKRSVQDPSPDYNQENV 108
DB 74 -NSSIADSEDPSESTSSSRRLPKRYFDDGYSPPPTKKRAAQRETPSDAEVEV 129
RESULT 8
A75634
McRB-related protein - Deinococcus radiodurans (strain R1)
C: Species: Deinococcus radiodurans
C: Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C: Accession: A75634
R: White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaleski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A: Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A: Reference number: A75250; MUID: 20036896
A: Accession: A75634
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-969 <WHI>
A: Cross-references: GB: AE001826; MID: g6460827; PIDN: AAF12568.1; PID: g6460864; TIGR: DR
A: Experimental source: strain R1
C: Genetics:
A: Gene: DRB0143
A: Map position: megaplasmid
A: Genome: plasmid
A: Note: plasmid MP1

Query Match 11.4%; Score 70; DB 2; Length 969;
Best Local Similarity 26.4%; Pred. No. 48;
Matches 33; Conservative 13; Mismatches 55; Indels 24; Gaps 4;

QY 7 FTAILAFSLAOSFGAVCKEPQEYVPGGGRKRPDLYQ-----DPDLY-QLLQRLFKS 53
DB 368 FGALFLPLPGREAAQAQLOQYMSGVGRSRLRVGLSLLEHLESDKPELDAALTY 427

QY 54 HSSLEGLKALSOXSTDPKESTSPEKRDHDFVFXGCKRSVQDPSPDYNQENVPSFGI 113
DB 428 LDALVDLLDGLMR-----PSEETSTEE-----ICVPGTRPVAPTAFAFVPGVPLNQLI 476

QY 114 LKYP 118
DB 477 LYGPP 481

RESULT 9
T26767
hypothetical protein Y39G8B.b - Caenorhabditis elegans
C: Species: Caenorhabditis elegans
C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C: Accession: T26767
R: Smye, R.
submitted to the EMBL Data Library, September 1999
A: Reference number: Z20262
A: Accession: T26767
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-437 <WIL>
A: Cross-references: EMBL: AL110482; MID: e1542197; PIDN: CAB54386.1; CESP: Y39G8B.b
A: Experimental source: clone Y39G8B
C: Genetics:
A: Gene: CESP: Y39G8B.b
A: Introns: 12/2; 87/3; 265/3

Query Match 11.3%; Score 69.5; DB 2; Length 437;
Best Local Similarity 27.8%; Pred. No. 22;
Matches 22; Conservative 13; Mismatches 33; Indels 11; Gaps 4;

QY 32 PGGG---RSKRDPDLY---QLLQRLFKSHSSLE-----GLLKALSOXSTDPKESTSPEKRD 81

Db 237 PGSALYRKHDNPDLNLYNETLQSIAGHGKLELKPCKLKPCKLKPCKPKPKKH 296
QY 82 MHDFVFGXMGKRSVQDPS 100
Db 297 KHNRTGT-AEKSKKPENP 314

RESULT 10
S35160
aspartate kinase (EC 2.7.2.4) / homoserine dehydrogenase (EC 1.1.1.3) precursor - carrot
C:Species: Daucus carota (carrot)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C:Accession: S35160; S38836
R:Weismann, J.M.; Matthews, B.F.
Plant Mol. Biol. 22, 301-312, 1993
A:Title: Identification and expression of a cDNA from Daucus carota encoding a bifunctional
A:Reference number: S35160; MUID:93283634
A:Accession: S35160
A:Molecule type: mRNA
A:Residues: 1-921 <WE1>
A:Cross-references: EMBL:L11529; NID:9167547; PIDN:AAA16972.1; PID:g464225
A:Accession: S38836
A:Molecule type: protein
A:Residues: 338-358; 405-433, 'S', 435-437; 698-726, 739, 'A', 740-741, 'LGSPS' <WE2>
C:Superfamily: thra bifunctional enzyme; aspartate kinase homology; homoserine dehydroge
C:Keywords: chloroplast; multifunctional enzyme; oxidoreductase; phosphotransferase
F:92-557/Domain: aspartate kinase homology <DK1>
F:560-818/Domain: homoserine dehydrogenase homology <HSD>
F:564-592/Region: beta-alpha-beta NAD(P) nucleotide-binding fold

Query Match 11.3%; Score 69; DB 2; Length 921;
Best Local Similarity 31.2%; Pred. No. 57;
Matches 29; Conservative 12; Mismatches 42; Indels 10; Gaps 3;
QY 30 VVPGGSRKRDPLYLQRLFKSHSLE-GLLKALSQXSTDPKESTSPKRDHDFVVG 88
Db 243 VVNPAGSNQVDPVLESEKLEKWFSSNQCTIVATGFIATQNTPTTLKRGDSFSA 302
QY 89 XMGK--RSVQDPSPTDVNQENVPFSGILKYPPR 119
Db 303 IMGALLRAGQVTIWDVN-----GYVSADPR 328

RESULT 11
JC4019
DNA mismatch repair protein rep-3 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 01-Dec-2000
C:Accession: JC4019; C32495; B32495
R:Liu, K.; Niu, L.; Linton, J.P.; Crouse, G.F.
Gene 147, 169-177, 1994
A:Title: Characterization of the mouse Rep-3 gene: Sequence similarities to bacterial an
A:Reference number: JC4019; MUID:95011610
A:Accession: JC4019
A:Molecule type: mRNA
A:Residues: 1-1126 <LIU>
A:Cross-references: GB:L10295
R:Linton, J.P.; Yen, J.Y.J.; Selby, E.; Chen, Z.; Chinsky, J.M.; Liu, K.; Kellems, R.E.;
Mol. Cell. Biol. 9, 3058-3072, 1989
A:Title: Dual bidirectional promoters at the mouse dhfr locus: cloning and characterizat
A:Reference number: A32495; MUID:89384567
A:Accession: C32495
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 47-60 <LIN>
A:Cross-references: GB:M24918; GB:J04244
A:Accession: B32495
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 47-440 <LI2>
A:Cross-references: GB:M24919; NID:g200703; PIDN:AAA40051.1; PID:g200704; GB:J04244

C:Genetics:
A:Gene: Rep-3
A:Introns: 86/2; 159/3; 222/3; 261/3; 301/1; 349/3; 405/2; 443/2; 481/1; 546/2; 650/2
A:Note: gene previously known as Rep-1
C:Keywords: DNA binding

Query Match 11.2%; Score 68.5; DB 2; Length 1126;
Best Local Similarity 29.3%; Pred. No. 81;
Matches 29; Conservative 8; Mismatches 41; Indels 21; Gaps 5;
QY 32 PGGGRSRKRDPLYLQRLFKSHSLEGLLKALSQXSTDPKESTSPKRD--MHDFV-- 87
Db 16 PGGRQ-----TVLSRFRFSAGLSR-----SASSTPAEKMFPTLAGNVSHLFRVTE 63
QY 88 GXMGKRSVQDPSPTDVNQENVP-----SFGILKYPPRAE 121
Db 64 GDSRKRSGLNGGPTKKKARKVPEKEENISVASHHPEAK 102

RESULT 12
B44502
nonstructural protein - Chandipura virus (strain I653514)
C:Species: Chandipura virus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: B44502
R:Wasters, P.S.; Banerjee, A.K.
Virology 157, 298-306, 1987
A:Title: Sequences of Chandipura virus N and NS genes: evidence for high mutability o
A:Reference number: A44502; MUID:87151129
A:Accession: B44502
A:Molecule type: mRNA
A:Residues: 1-293 <MAS>
A:Cross-references: GB:M16608; NID:g336043; PIDN:AAA48451.1; PID:g336045
C:Genetics:
A:Gene: NS
C:Superfamily: vesicular stomatitis virus nonstructural protein
C:Keywords: nonstructural protein

Query Match 11.1%; Score 68; DB 1; Length 293;
Best Local Similarity 23.9%; Pred. No. 19;
Matches 17; Conservative 15; Mismatches 37; Indels 2; Gaps 1;
QY 40 DPDLYLQRLFKSHSLEGLLKALSQXSTDPKESTSPKRDHDFVVGXMGKRSVQDPS 99
Db 3 DSQLYALKNYPKQLQDTLDSIENLEDDTKSEFSGSGSPTEGIPSYLAELDECEEDS 62
QY 100 PFDVNQENVPS 110
Db 63 EED--DDNLPT 71

RESULT 13
S72266
translation initiation factor eIF2B gamma chain - rat
N:Alternate names: guanine nucleotide-exchange protein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 31-Mar-2000
C:Accession: S72266
R:Price, N.T.; Kimball, S.R.; Jefferson, L.S.; Proud, C.G.
Biochem. J. 318, 631-636, 1996
A:Title: Cloning of cDNA for the gamma-subunit of mammalian translation initiation fa
A:Reference number: S72265; MUID:96404916
A:Accession: S72266
A:Molecule type: mRNA
A:Residues: 1-452 <PRI>
A:Cross-references: EMBL:U38253; NID:91537014; PIDN:AAC52788.1; PID:gl537015
A:Experimental source: strain Sprague-Dawley
C:Complex: heteropentamer; alpha, beta, gamma, delta and epsilon chain
C:Function:
A:Description: responsible for recycling initiation factor eIF2 to its active GTP-bou
A:Pathway: protein biosynthesis

C;Keywords: blocked amino end; GTP; protein biosynthesis
F;107/Binding site: magnesium (Asp) #status predicted

	Query Match	11.1%	Score 68;	DB 2;	Length 452;	
	Best Local Similarity	27.4%;	Pred. No. 32;			
	Matches 23;	Conservative	19;	Mismatches	37;	Indels 4; Gaps 3;
Qy	40	DPDYLQLRLRFKSHSSUGLLLKALSOXSTDPKESTSPEKR--DMHDFP-VGXMGKRVSQ	96			
		: : : : : : : : : : : : : : : : : : : :				
Db	111	DVALHVVD-LFRAYDASLAMLMRKGOSTEPVPGQGKKKTVEQRDFIGVDSTGKRLLF	169			
		: : : : : : : : : : : : : : : : : : : :				
Qy	97	PDSPDTDVNQENVPFGILKYPPR	119			
		: : : : : : : : : : : : : : : : : : : :				
Db	170	MANEADLDEELVIKGSIILOKHPR	192			

RESULT 14

G86185
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G86185
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: G86185
A:Status: preliminary
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-808 <STO>
A:Cross-references: GB:AE005172; NID:g2388582; PIDN:AAB71463.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

```

Query Match      11.1%; Score 68; DB 2; Length 808;
Best Local Similarity 28.6%; Pred. No. 62;
Matches 26; Conservative 17; Mismatches 34; Indels 14; Gaps 4;

Qy 10 ILAFSLAQSGF-----AVCKPQEEVVP-----GGRSK--RDPDLYQLLQRLFKS--HS 55
      |||      |||      |||      |||      |||      |||      |||      |||
Db 536 IRAFTVRLCKDVEAVRKEMRDNVPVSYSGSGGPKSIKRPKNLEETLRLLSLKPD 595

Qy 56 SLEGLLKALSOXSTDPKESTSPERKMDHDF 86
      :| :|||:: : :|||:: :
Db 596 TFOGAIKAINIKLALLDDSGRGVDMGFY 626

```

RESULT 15
T47340
hypothetical protein T21C14.40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 28-Jul-2000
C:Accession: T47340
R:Delseny, M.; Berger, C.; Cooke, R.; Gaubier, P.; Grellet, F.; Laudie, M.; Mewes, H.W.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24462
A:Accession: T47340
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-906
A:Cross-references: EMBL:AL138639
A:Experimental source: cultivar Columbia; BAC clone T21C14
C:Genetics:

A; Map position: 3
A; Introns: 90/1; 135/3; 152/3; 323/2; 408/3; 432/3; 456/3; 478/3; 500/3; 520/3
A; Note: T21C14.40
C; Superfamily: Arabidopsis thaliana hypothetical protein T21C14.40

	Query Match	11.18	Score 68;	DB 2;	Length 906;	
	Best Local Similarity	28.66;	Pred. No. 71;			
	Matches 2;	Conservative	10;	Mismatches	29;	Indels 16; Gaps
QY	33	GGGSKRRDPLYQLLRFLKSHSLEGL--LKALSQXSTDPKESTSPKPRMDHDFVCGXM	90			
			:	:	:	:
Db	295	GGVRKH-----QRPITEGGSSGVVSMEISIRIKDPANGTSRPPKDVDP-----	340			
QY	91	GKRSVQPDSPSTDVNQEN	107			
Db	341	GTRGVSPSKDMGCSDGN	357			

Search completed: May 3, 2002, 12:24:47
Job time: 114 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 12:24:08 ; Search time 11.63 Seconds
(without alignments)
381.466 Million cell updates/sec

Title: US-09-852-659-85

Perfect score: 613

Sequence: 1 MR1MLFTAILAFSLAOSFG.....DVNOENVSPGILKYPPRAE 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	407.5	66.5	126	1	TKNK_BOVIN
2	364.5	59.5	116	1	TKNK_MOUSE
3	344.5	56.2	116	1	TKNK_RAT
4	77	12.6	2211	1	FAS_BOVIN
5	72.5	11.8	237	1	AKH1_MOUSE
6	69	11.3	921	1	AKH1_MOUSE
7	68	11.1	293	1	RRPP_CHAV
8	68	11.1	452	1	E2B2_RAT
9	67.5	11.0	978	1	SIR3_YEAST
10	67	10.9	513	1	PIX1_DROME
11	67	10.9	823	1	YRR2_CAEEL
12	66.5	10.8	1091	1	MSH3_MOUSE
13	66.5	10.8	2353	1	CCAH_HUMAN
14	66	10.8	168	1	ARPL_CAEEL
15	66	10.8	201	1	SDC2_RAT
16	66	10.8	343	1	MAT2_COCHE
17	66	10.8	927	1	B3AT_RAT
18	65.5	10.7	911	1	B3AT_HUMAN
19	65	10.6	282	1	PE11_YEAST
20	64.5	10.5	910	1	DNJM_MYCPN
21	64.5	10.5	1005	1	P532_HUMAN
22	64.5	10.5	1374	1	VCAP_HSV11
23	64.5	10.5	2464	1	MAP2_MOUSE
24	64	10.4	198	1	ABP1_SACEX
25	63.5	10.4	198	1	GB11_CANFA
26	63.5	10.4	355	1	CXA5_RAT
27	63.5	10.4	515	1	NCAP_P13B
28	63	10.3	130	1	TKNL_MESAU
29	63	10.3	307	1	CIW7_HUMAN
30	63	10.3	356	1	E2F3_MOUSE
31	63	10.3	465	1	E2F3_HUMAN
32	63	10.3	1270	1	DDX9_HUMAN
33	62.5	10.2	281	1	EF1D_MOUSE

ALIGNMENTS

RESULT 1

TKNK_BOVIN

ID TKNK_BOVIN STANDARD; PRT; 126 AA.

AC P08858;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE NEUROKININ B PRECURSOR (NEUROMEDIN K).

GN TAC3 OR NKNB OR NKB.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_Taxid=9913;

RN [1]

RP MEDLINE=66313713; PubMed=3462746;

RA Kotani H., Hoshimaru M., Nawa H., Nakanishi S.;

RT "Structure and gene organization of bovine neuromedin K precursor.";

Proc. Natl. Acad. Sci. U.S.A. 83:7074-7078(1986).

CC FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,

CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND

CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH

CC MUSCLES.

CC SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

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EMBL; M14351; AAA30723.1; JOINED.

EMBL; M14347; AAA30723.1; JOINED.

EMBL; M14348; AAA30723.1; JOINED.

EMBL; M14349; AAA30723.1; JOINED.

EMBL; M14350; AAA30723.1; JOINED.

PIR; A25905; A25905.

InterPro: IPR003635; Neurokinin.

InterPro: IPR002040; Tachykinin.

ProDom: PD020370; Neurokinin.1.

PROSITE: PS00267; TACHYKININ; 1.

Tachykinin; Neuropeptide; Cleavage on pair of basic residues;

Amidation; signal.

SIGNAL 1 20 POTENTIAL.

PEPTIDE 86 95 NEUROKININ B.

MOD.RES 95 95 AMIDATION (G-96 PROVIDE AMIDE GROUP).

SEQUENCE 126 AA; 13871 MW; 446EF433498EC059 CRC64;

Query Match

Best Local Similarity 64.3%; DB 1; Length 126;

Matches 81; Conservative 15; Mismatches 25; Indels 5; Gaps 2;

```

QY 1 MRIMLFTAILAFSLAQSGAVCKEPEQEVVPGGSKRDPDLYQ-----LLQRLFKSH-S 55
Db 1 MRSTLLFAVILALSSARSLGAVCEEQVVPVGGGSKDNLQPLPSLLRLLYDSRVV 60
QY 56 SLEGLLKALSOXSTDPKSTSPKRDHDFVFXMGKRSVQPDSPDVTQNVQENVPSPFGILK 115
Db 61 SLQGLLKALSKASVGPKEPQLPKRDMHDFVFLGMLGRNLQPDPTPDVQENIPSPFGTFK 120
QY 116 YPPRAE 121
Db 121 YPPSVE 126

RESULT 2
TKNK_MOUSE
ID TKNK_MOUSE STANDARD; PRT; 116 AA.
AC P55099;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NEUROKININ B PRECURSOR (NEUROMEDIN K) (PREPROTACHYKININ B) (PPT-B).
GN TAC3 OR NKNB OR TAC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Brain;
RA Koko K., Muneata E., Hosaka M., Murakami K., Nakayama K.;
RT "Cloning and sequence analysis of mouse cDNAs encoding
  preprotachykinin A and B.";
RL Biomed. Res. 14:253-259(1993).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D14423; BAA03316.1; -
CC MGD; MGI:98476; Tac2.
CC InterPro; IPR003635; Neurokinin.
CC ProDom; PD020370; Neurokinin; 1.
CC PROSITE; PS00267; TACHYKININ; 1.
CC Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
CC Amidation; Signal.
CC SIGNAL 1 20 POTENTIAL.
CC PEPTIDE 82 91 NEUROKININ B.
CC MOD_RES 91 91 AMIDATION (G-92 PROVIDE AMIDE GROUP).
CC SEQUENCE 116 AA; 12809 MW; BF6E89373E2031CC CRC64;
CC -----
CC Query Match 59.5%; Score 364.5; DB 1; Length 116;
CC Best Local Similarity 63.3%; Pred. No. 1.7e-29;
CC Matches 76; Conservative 15; Mismatches 20; Indels 9; Gaps 3;

QY 1 MRIMLFTAILAFSLAQSGAVCKEPEQEVVPGGSKRDPDLYQ-----LLQRLFKSH-S 55
Db 1 MRSAMLFAVLAALSLAWTFGAVCEEPQEQ-----GGRLSKDSDLYQLPPSLRLLYDSRVV 56
QY 56 SLEGLLKALSOXSTDPKSTSPKRDHDFVFXMGKRSVQPDSPDVTQNVQENVPSPFGILK 115
Db 57 SLEGLLKALSKASVGPKEPQLPKRDMHDFVFLGMLGRNLQPDPTPDVQENIPSPFGILK 116

RESULT 4
FA5_BOVIN
ID FA5_BOVIN STANDARD; PRT; 2211 AA.
AC Q28107; Q28108;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).
GN F5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

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```

RESULT 3
TKNK_RAT
ID TKNK_RAT STANDARD; PRT; 116 AA.
AC P08435;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NEUROKININ B PRECURSOR (NEUROMEDIN K).
GN TAC3 OR NKNB OR NKB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88051833; PubMed=3479225;
RA Bonner T.I., Affolter H.-U., Young A.C., Young W.S. III;
RT "A cDNA encoding the precursor of the rat neuropeptide, neurokinin
  B.";
RL Brain Res. 388:243-249(1987).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC -----
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CC -----
CC EMBL; M16410; AAA41711.1; -
CC FIR; A43779; A43779.
CC InterPro; IPR003635; Neurokinin.
CC ProDom; PD020370; Neurokinin; 1.
CC PROSITE; PS00267; TACHYKININ; 1.
CC Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
CC Amidation; Signal.
CC SIGNAL 1 20 POTENTIAL.
CC PEPTIDE 82 91 NEUROKININ B.
CC MOD_RES 91 91 AMIDATION (G-92 PROVIDE AMIDE GROUP).
CC SEQUENCE 116 AA; 12659 MW; C73EC67F2BAF8C8C CRC64;
CC -----
CC Query Match 56.2%; Score 344.5; DB 1; Length 116;
CC Best Local Similarity 60.0%; Pred. No. 1.6e-27;
CC Matches 72; Conservative 16; Mismatches 23; Indels 9; Gaps 3;

QY 1 MRIMLFTAILAFSLAQSGAVCKEPEQEVVPGGSKRDPDLYQ-----QLQRLFKSH-S 55
Db 1 MRSAMLFAVLAALSLAWTFGAVCEEPQEQ-----GGRLSKDSDLYQLPPSLRLLYDSRSI 56
QY 56 SLEGLLKALSOXSTDPKSTSPKRDHDFVFXMGKRSVQPDSPDVTQNVQENVPSPFGILK 115
Db 57 SLEGLLKALSKASVGPKEPQLPKRDMHDFVFLGMLGRNLQPDPTPDVQENIPSPFGILK 116

RESULT 4
FA5_BOVIN
ID FA5_BOVIN STANDARD; PRT; 2211 AA.
AC Q28107; Q28108;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).
GN F5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

```


CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92147638; PubMed=1737753;
 RA Guineto E.R., Esmon C.T., Mann K.G., Macgillivray R.T.;
 RL "The complete cDNA sequence of bovine coagulation factor V.";
 RT J. Biol. Chem. 267:2971-2978(1992).
 CC -1- FUNCTION: COAGULATION FACTOR V IS A COFACTOR THAT PARTICIPATES
 CC WITH FACTOR XA TO ACTIVATE PROTHROMBIN TO THROMBIN.
 CC -1- SUBUNIT: FACTOR VA IS COMPOSED OF AN HEAVY CHAIN AND OF A LIGHT
 CC CHAIN NONCOVALENTLY BOUND. THE INTERACTION BETWEEN THE TWO CHAINS
 CC IS CALCIUM-DEPENDENT.
 CC -1- DOMAIN: DOMAIN B CONTAINS 29.5 X 9 AA TANDEM REPEATS, AND 2 X 17
 CC AA REPEATS.
 CC -1- PTM: THROMBIN ACTIVATES FACTOR V PROTEOLYTICALLY TO THE ACTIVE
 CC COFACTOR, FACTOR V(A) (FORMATION OF A HEAVY CHAIN AT THE N-
 CC TERMINUS AND A LIGHT CHAIN AT THE C-TERMINUS).
 CC -1- PTM: SULFATION IS REQUIRED FOR EFFICIENT THROMBIN CLEAVAGE AND
 CC ACTIVATION AND FOR FULL PROCOAGULANT ACTIVITY (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 3 F5/8 TYPE A DOMAINS; EACH IS COMPOSED OF
 CC 2 PLASTOCYANIN-LIKE REPEATS.
 CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
 CC -1- SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
 CC -----
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 CC -----
 DR EMBL; M81440; AAA30512.1; -;
 DR EMBL; M81441; AAA30513.1; -;
 DR HSP; P00450; 1KCW.
 DR InterPro; IPR001117; Cu-oxidase.
 DR InterPro; IPR000421; FA58_C.
 DR Pfam; PF00394; Cu-oxidase; 3.
 DR Pfam; PF00754; F5_F8_type_C; 2.
 DR SMART; SM00231; FA58C; 2.
 DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.
 DR PROSITE; PS01285; FA58C_1; 2.
 DR PROSITE; PS01286; FA58C_2; 2.
 KW Blood coagulation; Plasma; Glycoprotein; Sulfation; Calcium; Signal;
 KW Zymogen; Repeat.
 FT SIGNAL 1 28
 FT CHAIN 29 2211 POTENTIAL.
 FT CHAIN 29 741 COAGULATION FACTOR V.
 FT PEPTIDE 742 1564 HEAVY CHAIN (BY SIMILARITY).
 FT ACTIVATION PEPTIDE (CONNECTING REGION)
 FT (BY SIMILARITY).
 FT LIGHT CHAIN (BY SIMILARITY).
 FT F5/8 TYPE A 1.
 FT PLASTOCYANIN-LIKE 1.
 FT PLASTOCYANIN-LIKE 2.
 FT F5/8 TYPE A 2.
 FT PLASTOCYANIN-LIKE 3.
 FT PLASTOCYANIN-LIKE 4.
 FT B.
 FT TO 17 AA REPEATS IN HUMAN FA5.
 FT 2 X 14 AA TANDEM REPEATS.
 FT 1.
 FT 2.
 FT 30 X 9 AA TANDEM REPEATS OF [AS]-L-S-P-
 FT D-[LP]-[GS]-Q-[TE] (APPROXIMATE).
 FT 1.
 FT 2.
 FT 3.
 FT 4.
 FT 5.
 FT 6.

FT REPEAT 1242 1250
 FT REPEAT 1251 1258
 FT REPEAT 1260 1268
 FT REPEAT 1269 1277
 FT REPEAT 1278 1286
 FT REPEAT 1287 1295
 FT REPEAT 1296 1304
 FT REPEAT 1305 1313
 FT REPEAT 1314 1322
 FT REPEAT 1323 1331
 FT REPEAT 1332 1340
 FT REPEAT 1341 1349
 FT REPEAT 1350 1358
 FT REPEAT 1359 1367
 FT REPEAT 1368 1376
 FT REPEAT 1377 1385
 FT REPEAT 1386 1394
 FT REPEAT 1395 1403
 FT REPEAT 1404 1412
 FT REPEAT 1413 1421
 FT REPEAT 1422 1430
 FT REPEAT 1431 1439
 FT REPEAT 1440 1444
 FT REPEAT 1445 1453
 FT DOMAIN 1569 1890
 FT DOMAIN 1569 1738
 FT DOMAIN 1748 1890
 FT DOMAIN 1894 2048
 FT DOMAIN 2053 2208
 FT SITE 741 742
 FT SITE 1034 1035
 FT SITE 1564 1565
 FT DISULFID 167 193
 FT DISULFID 499 525
 FT DISULFID 1712 1738
 FT DISULFID 1894 2048
 FT DISULFID 2053 2208
 FT MOD_RES 701 701
 FT MOD_RES 730 730
 FT MOD_RES 1513 1513
 FT MOD_RES 1529 1529
 FT MOD_RES 1537 1537
 FT MOD_RES 1541 1541
 FT CARBOHYD 225 225
 FT CARBOHYD 239 239
 FT CARBOHYD 297 297
 FT CARBOHYD 382 382
 FT CARBOHYD 460 460
 FT CARBOHYD 553 553
 FT CARBOHYD 587 587
 FT CARBOHYD 745 745
 FT CARBOHYD 756 756
 FT CARBOHYD 774 774
 FT CARBOHYD 780 780
 FT CARBOHYD 902 902
 FT CARBOHYD 952 952
 FT CARBOHYD 964 964
 FT CARBOHYD 1044 1044
 FT CARBOHYD 1053 1053
 FT CARBOHYD 1062 1062
 FT CARBOHYD 1071 1071
 FT CARBOHYD 1078 1078
 FT CARBOHYD 1094 1094
 FT CARBOHYD 1451 1451
 FT CARBOHYD 1490 1490
 FT CARBOHYD 1550 1550
 FT CARBOHYD 1890 1890
 FT CARBOHYD 1839 1839
 FT CARBOHYD 1997 1997
 FT CARBOHYD 2196 2196
 FT VARIANT 587 592
 FT NETLPA -> T (IN VARIANT 2).
 SQ SEQUENCE 2211 AA; 248981 MW; CBBF90B738667C45 CRC64;

```
Query Match      12.6%; Score 77; DB 1; Length 2211;
Best Local Similarity 28.6%; Pred. No. 14;
Matches 32; Conservative 13; Mismatches 39; Indels 28; Gaps 6;

QY 14 SLAQSGAVCKEP---QEEVPGGGRKRDPLYQ-----LLQRLFKSHSLEGLLKAL 64
DQ 1269 SLSPDLGQTALSPDPCQESLPDLGQTSLSPDLSPDLGQTALSPDPQESLSPDL 1328
QY 65 SQXSTDP---KSTSPKRDHDFVVGXMGKRSVQDPTDQNVN-PSFG 112
DQ 1329 GQTALSPDPSQESLSPD-----LGQTSLSLSP-----DLGQESLSPDLG 1365

RESULT 5
HK31_MOUSE
ID HK31_MOUSE STANDARD; PRT; 237 AA.
AC P97436; O09087;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HOMEOBOX PROTEIN NKX-3.1.
GN NKX3A OR NKX-3.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=97112961; PubMed=8943214;
RA Biebrich C.J., Fujita K., He W.-W., Jay G.;
RT "Prostate-specific and androgen-dependent expression of a novel
RT homeobox gene."
RL J. Biol. Chem. 271:31779-31782(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS WEBSTER;
RX MEDLINE=97287410; PubMed=9142502;
RA Scialvolino P.J., Abrams E.W., Yang L., Austenberg L.P., Shen M.M.,
RA Abate-Shen C.;
RT "Tissue-specific expression of murine Nkx3.1 in the male urogenital
RT system."
RL Dev. Dyn. 209:127-138(1997).
CC -!- FUNCTION: MAY FUNCTION IN THE GROWTH AND DEVELOPMENT OF THE
CC PROSTATE AND/OR OTHER TISSUES OF THE MALE UROGENITAL SYSTEM AND
CC MAY PLAY A ROLE IN SEXUALLY DIMORPHIC AS WELL AS NON-SEXUALLY
CC DIMORPHIC ORGANOGENESIS. MAY FUNCTION AS A TRANSCRIPTION FACTOR
CC AND PLAY A PROMINENT ROLE BOTH IN THE INITIATION OF PROSTATE
CC DEVELOPMENT AND IN THE MAINTENANCE OF THE DIFFERENTIATED STATE OF
CC PROSTATIC EPITHELIAL CELLS.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE MALE UROGENITAL SYSTEM,
CC INCLUDING THE TESTIS, SEMINAL VESICLE, AND THE PROSTATE AND ALSO
CC IN THE DORSAL AORTA AND KIDNEY. EXPRESSION IS ELEVATED IN SEXUALLY
CC MATURE MALES.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE MALE UROGENITAL SYSTEM
CC DURING LATE EMBRYOGENESIS AND ADULTHOOD. AT DAY 14.5, EXPRESSED IN
CC THE DEVELOPING UROGENITAL SINUS, AND AT DAY 17.5 IN THE VENTRAL
CC PROSTATIC BUDS. FOUND IN THE DEVELOPING TESTIS AT DAYS 14.5 AND
CC 17.5 OF GESTATION, AND ALSO EXPRESSED AT DAY 14.5 IN THE
CC ENDOTHELIAL CELLS THAT LINE THE DORSAL AORTA WHICH ARE IN
CC PROXIMITY TO THE DEVELOPING METANEPHRIC KIDNEYS.
CC -!- INDUCTION: STIMULATED BY ANDROGEN.
CC -!- SIMILARITY: BELONGS TO THE NK-3 FAMILY OF HOMEOBOX PROTEINS.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; U73460; AAC52956.1; -
CC EMBL; U88542; AAB58025.1; -
CC HSSP; P23441; 1FTT.
CC MGD; MGI:97352; Nkx3-1.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PRO0024; HOMEOBOX.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEOBOX_1; 1.
CC PROSITE; PS00071; HOMEOBOX_2; 1.
CC Homeobox; DNA-binding; Nuclear protein.
CC DNA_BIND 125 184 HOMEOBOX.
CC SEQUENCE 237 AA; 26824 MW; 4B074387F3BA1223 CRC64;

Query Match      11.8%; Score 72.5; DB 1; Length 237;
Best Local Similarity 27.3%; Pred. No. 3.4;
Matches 24; Conservative 10; Mismatches 35; Indels 19; Gaps 3;

QY 25 EPOEEVVGGR-----SKRDPDLYQLQRLFKSHSLEGLLKALSQXSTDPKEST 75
DQ 6 EPREPRVEAGGRSFWAAPTQSKRLTSF--LIQDILDRARHGHSNGNQSPDPRDS 63
QY 76 SPEKRDHDFVVGXMGKRSVQDPTDV 103
DQ 64 APEP-----DKAGRGVAPEDPPSI 83

RESULT 6
AKH_DAUCA
ID AKH_DAUCA STANDARD; PRT; 921 AA.
AC P37142;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BIFUNCTIONAL ASPARTOKINASE/HOMOSERINE DEHYDROGENASE, CHLOROPLAST
DE PRECURSOR (AK-HD) (AK-HSDH) [INCLUDES: ASPARTOKINASE (EC 2.7.2.4);
DE HOMOSERINE DEHYDROGENASE (EC 1.1.1.3)] (FRAGMENT).
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=93283634; PubMed=8507831;
RA Weismann J.M., Matthews B.F.;
RT "Identification and expression of a cDNA from Daucus carota encoding
RT a bifunctional aspartokinase-homoserine dehydrogenase."
RL Plant Mol. Biol. 22:301-312(1993).
CC -!- CATALYTIC ACTIVITY: L-HOMOSERINE + NAD(P)(+) = L-ASPARTATE
CC BETA-SEMIALDEHYDE + NAD(P)H.
CC -!- CATALYTIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSPHO-L-
CC ASPARTATE.
CC -!- PATHWAY: CATALYZES 2 NONCONSECUTIVE REACTIONS IN THE COMMON
CC BIOSYNTHETIC PATHWAY LEADING FROM ASP TO DIAMINOPIMELATE AND LYS,
CC TO MET, AND TO THR AND ILE.
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
CC ASPARTOKINASE FAMILY.
CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE
CC HOMOSERINE DEHYDROGENASE FAMILY.
CC
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EMBL; L11529; AAA16972.1; -
DR
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DR PIR: S35160; S35160.
DR InterPro: IPR002912; ACT.
DR InterPro: IPR001048; Akinase.
DR InterPro: IPR001341; Aspartokinase.
DR InterPro: IPR001342; Homoserine_dh.
DR Pfam: PF00696; akinase; 1.
DR Pfam: PF01842; ACT; 2.
DR Pfam: PF00742; Homoserine_dh; 1.
DR PROSITE: PS00324; ASPARTOKINASE; 1.
DR PROSITE: PS01042; HOMOSER_DHGENSE; 1.
DR Transferrase; Kinase; Oxidoreductase; Methionine biosynthesis; NADP;
KW Multifunctional enzyme; Chloroplast; transit peptide.
FT NON_TER 1
FT TRANSIT <1 87
FT CHAIN 88 921
FT CLOROPLAST.
FT BIFUNCTIONAL ASPARTOKINASE/HOMOSERINE
FT DEHYDROGENASE.
FT ASPARTOKINASE.
FT DOMAIN ?
FT DOMAIN ?
FT DOMAIN ? 921
FT NP_BIND ?
FT NADP (POTENTIAL).
SQ SEQUENCE 921 AA; 100226 MW; 9C89C392DA76A996 CRC64;

Query Match 11.3%; Score 69; DB 1; Length 921;
Best Local Similarity 31.2%; Pred. No. 34;
Matches 29; Conservative 12; Mismatches 42; Indels 10; Gaps 3;

QY 30 VVPGGSRKRDPLLYQLLQRLFKSHSLLE-GLLKALSOXSTDPKSTSPKRDMDHDFVVG 88
DB 243 VVNPAGSNQVDPDLYSEKRLKWKFNSSNOCQIVATGFIASIPQNTTLKRDGSDFSRA 302

QY 89 XMKGK--RSVQPSPTDVNQENVPFGILKYPPR 119
DB 303 IMGALLRAGQVTIWDVN-----GVISADPR 328

RESULT 7
RRPP_CHAV STANDARD; PRT; 293 AA.
AC P16380;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE 13-DEC-1998 (Rel. 37, Last annotation update)
DE RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.48) (NONSTRUCTURAL
DE PHOSPHOPROTEIN).
GN NS.
OS Chandipura virus (strain I653514).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11273;
RN [1]
SEQUENCE FROM N.A.
DR MEDLINE=87151129; PubMed=3029973;
RA Masters P.S., Banerjee A.K.;
RT "Sequences of Chandipura virus N and NS genes: evidence for high
RT mutability of the NS gene within vesiculoviruses.";
RL Virology 157:298-306(1987).
CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC POLYMERASE. IT MAY FUNCTION IN TEMPLATE BINDING.
CC
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CC
CC EMBL: M16608; AAA48451.1; -
DR PIR: B44502; B44502.
DR InterPro: IPR000224; Viral phospho.
DR Pfam: PF00922; Phosphoprotein; 1.
KW Transferase; RNA-directed RNA polymerase; Phosphorylation;

KW Nonstructural protein.
SQ SEQUENCE 293 AA; 32523 MW; 8CB7D36EBA67A26C CRC64;

Query Match 11.1%; Score 68; DB 1; Length 293;
Best Local Similarity 23.9%; Pred. No. 12;
Matches 17; Conservative 15; Mismatches 37; Indels 2; Gaps 1;

QY 40 DPDIYQLLQRLFKSHSLLEGLLKALSOXSTDPKSTSPKRDMDHDFVVGXMGKRKSVQPS 99
DB 3 DSQLYQALKNYPKQLDPLDSTENLEDKTSKPSGSGPTGIPSYVYLAELDECEEDS 62

QY 100 PTDVQNQENVPS 110
DB 63 EED--DDNLEPT 71

RESULT 8
E2BG_RAT STANDARD; PRT; 452 AA.
ID E2BG_RAT
AC P70541;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP
DE EXCHANGE FACTOR).
DE
GN EIF2B3 OR EIF2BG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Skeletal muscle;
RX MEDLINE=96404916; PubMed=8809057;
RA Price N.T., Kimball S.R., Jefferson L.S., Proud C.G.;
RT "Cloning of cDNA for the gamma-subunit of mammalian translation
RT initiation factor 2B, the guanine nucleotide-exchange factor for
RT eukaryotic initiation factor 2.";
RL Biochem. J. 318:631-636(1996).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF EUKARYOTIC INITIATION FACTOR
CC 2-BOUND GDP FOR GTP.
CC -!- SUBUNIT: COMPLEX OF FIVE DIFFERENT SUBUNITS; ALPHA, BETA, GAMMA,
CC DELTA AND EPSILON.
CC -!- TISSUE SPECIFICITY: BRAIN, HEART, LIVER, MUSCLE AND TESTES.
CC -!- SIMILARITY: BELONGS TO THE EIF-2B GAMMA/EPSILON SUBUNITS FAMILY.
CC
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CC
CC EMBL: U38253; AAC52788.1; -
DR InterPro: IPR001825; NTP transferase.
DR Pfam: PF00483; NTP_transferase; 1.
KW Amino-acid biosynthesis; Translation regulation.
SQ SEQUENCE 452 AA; 50407 MW; 18314D39464233F9 CRC64;

Query Match 11.1%; Score 68; DB 1; Length 452;
Best Local Similarity 27.7%; Pred. No. 19;
Matches 23; Conservative 19; Mismatches 37; Indels 4; Gaps 3;

QY 40 DPDIYQLLQRLFKSHSLLEGLLKALSOXSTDPKSTSPKRDMDHDFVVGXMGKRKSVQ 96
DB 111 DVALHEVVD-LFRAYDASLAMLKRGKGGESTPEVPGKGKKTKVEQDFIGVDSTGKRLLF 169

QY 97 PDSPTDVNQENVPFGILKYPPR 119
DB 170 MANEADLDELVIKGSILQKHPR 192

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RESULT 9
SIR3_YEAST
ID SIR3_YEAST STANDARD; PRT; 978 AA.
AC P06701;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE REGULATORY PROTEIN SIR3 (SILENT INFORMATION REGULATOR 3).
GN SIR3 OR STE8 OR MAR2 OR CMT1 OR YLR442C OR L9753.10.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95126876; PubMed=6098447;
RA Shore D., Squire M., Nasmith K.A.;
RT "Characterization of two genes required for the position-effect
  control of yeast mating-type genes.";
RL EMBO J. 3:2817-2823(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
RA Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,
RA Wilcox L., Wohlman P., Vaudin M., Wilson R., Waterston R.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE PROTEINS SIR1 THROUGH SIR4 CONTROL THE EXPRESSION OF
  MATING TYPE GENES RESIDENT AT LOCI OF EITHER END OF CHROMOSOME
  III. SIR3 AND SIR4 ASSOCIATE WITH THE C-TERMINUS OF RAPI TO FORM A
  DNA-BINDING COMPLEX THAT INITIATES THE REPRESSION AT THE HM LOCI
  AND TELOMERES.
CC -1- SUBUNIT: INTERACTS WITH RAPI C-TERMINUS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X01420; CAA25668.1; -
CC EMBL; U21094; AAB67522.1; -
CC PIR; S05892; RGYB13.
CC SGD; S0004434; SIR3.
CC InterPro: IPR001025; BAH.
CC Pfam; PF01426; BAH; 1.
CC SMART; SM00439; BAH; 1.
CC Transcription regulation; Repressor; DNA-binding; Nuclear protein.
FT CONFLICT 331 331 P -> S (IN REF. 1).
FT CONFLICT 335 335 T -> P (IN REF. 1).
FT CONFLICT 405 405 S -> G (IN REF. 1).
FT CONFLICT 421 421 K -> Q (IN REF. 1).
FT CONFLICT 429 430 NE -> KK (IN REF. 1).
FT CONFLICT 497 497 L -> V (IN REF. 1).
FT CONFLICT 587 587 Q -> R (IN REF. 1).
FT CONFLICT 597 597 I -> V (IN REF. 1).
FT CONFLICT 669 669 E -> D (IN REF. 1).
FT CONFLICT 704 704 R -> G (IN REF. 1).
FT CONFLICT 712 712 S -> T (IN REF. 1).
FT CONFLICT 726 726 D -> N (IN REF. 1).
FT CONFLICT 828 828 L -> F (IN REF. 1).
FT CONFLICT 830 830 V -> L (IN REF. 1).
FT CONFLICT 925 925 Q -> K (IN REF. 1).
SQ SEQUENCE 978 AA; 111359 MW; CA2503D7645397AC CRC64;

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Query Match 11.0%; Score 67.5; DB 1; Length 978;
Best Local Similarity 23.2%; Pred. No. 51;
Matches 23; Conservative 17; Mismatches 36; Indels 23; Gaps 4;

QY 23 CKEPQEVVPGGSRKRDPLDYLQRLFKSH-SLEGLLKALQSXSTDPEKSTSPKRD 81
  | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 177 CEPTAEKFPV-----IDFIQIRRVKEMEPKQSDYELKRVSV-----PVSGQKTRQV 224
  | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : |
QY 82 MHDFVGVCMKGR-----SVQPSPTDVNOENVPS 110
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 225 MHKMGVERSSRLAKPKSMKKIKIEPSADDDVNGNIPS 263
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 10
PIXI_DROME
ID PIXI_DROME STANDARD; PRT; 513 AA.
AC O18400;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PITUITARY HOMEOBOX 1 HOMOLOG (D-PTX1).
GN PTX1.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98092108; PubMed=9431811;
RA Vorbruegg G., Constien R., Zillian O., Wimmer E.A., Dowe G.,
RA Taubert H., Noll M., Jaekle H.;
RT "Embryonic expression and characterization of a Ptx1 homolog in
  Drosophila.";
RL Mech. Dev. 68:139-147(1997).
CC -1- FUNCTION: MIGHT CONTROL PHYSIOLOGICAL CELL FUNCTIONS THAN PATTERN
  FORMATION DURING EMBRYOGENESIS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED IN THE POSTERIOR REGION OF
  THE BLASTODERM EMBRYO. IN LATER STAGES OF EMBRYONIC DEVELOPMENT,
  DETECTED IN THE POSTERIOR PORTION OF THE MIDGUT, IN THE
  DEVELOPING MALPIGHIAN TUBULES, IN A SUBSET OF VENTRAL SOMATIC
  MUSCLES, IN THE DEVELOPING CNS AND IN BOLWIG'S ORGAN.
CC -1- SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.
  "BICOID" SUBFAMILY.
CC -----
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CC -----
CC EMBL; AJ001519; CAA04801.1; -
CC FlyBase; FBgn0020912; ptx1.
CC InterPro: IPR001356; Homeobox.
CC InterPro: IPR003654; OAR_domain.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEOBOX.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEOBOX_1; 1.
CC PROSITE; PS00071; HOMEOBOX_2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
  Transcription regulation; Activator.
FT DOMAIN 119 126 POLY-SER.
FT DOMAIN 268 327 HOMEOBOX.
FT SEQUENCE 513 AA; 54804 MW; 3E6B5C19ECEB2E45 CRC64;
SQ

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Query Match 10.9%; Score 67; DB 1; Length 513;
Best Local Similarity 27.5%; Pred. No. 28;
Matches 30; Conservative 11; Mismatches 40; Indels 28; Gaps 6;

QY 20 GAVCKEPOEEVVGGRKRDPLQLQLQLF-----KSHSLLEGLLKA----- 63
DB 151 GGYSHPHHTVVP-PHTPKHEP-LEKLSLFFSWAETGDFRDHSHSTAVANSLDSTH 207
QY 64 LSQXSTDPKESPKRDMHDFVFGXMKRSQVDPSTDVNOENVPFSG 112
DB 208 LNNFOTSSSTISNRSRDKD-----GNRSV---NETTIKTENISSG 247

RESULT 11
YRR2_CAEEL
ID YRR2_CAEEL STANDARD; PRT; 823 AA.
AC Q09345;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 91.1 KDA PROTEIN R144.2 IN CHROMOSOME III.
GN R144.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Favello T.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: SOME, TO YEAST PCF11 AND S.POMBE SPAC4G9.04C.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; U23515; AAK21453.1; -
CC WormPep: R144.2; CE02032.
KW Hypothetical protein.
SQ SEQUENCE 823 AA; 91142 MW; 18654DB4740FC06A CRC64;

Query Match 10.9%; Score 67; DB 1; Length 823;
Best Local Similarity 26.7%; Pred. No. 47;
Matches 28; Conservative 15; Mismatches 36; Indels 26; Gaps 5;

QY 17 QSGFAYCKEPOEEVVGGRKRDPLQLQLRKFHSHSLLEGLLKALSOXSTDP---KE 73
DB 205 KSGPTVNEKQVKKP-----KQDP-----LKLFPSSA-----SKTSSSPAGLKR 246
QY 74 STSPKRDHDFVFGXMKRSQVDPSTDVNOENVPFSGILKYPP 118
DB 247 KSPASEHPN-----APIRKKPQPPKQPTAIDEDLRSISLTKKPP 286

RESULT 12
MSH3_MOUSE
ID MSH3_MOUSE STANDARD; PRT; 1091 AA.
AC P13705;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE DNA MISMATCH REPAIR PROTEIN MSH3 (REPAIR-3 PROTEIN) (REP-1).
GN MSH3 OR REP-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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FT TRANSMEM 1752 1772 S5-OF REPEAT IV (POTENTIAL).
FT DOMAIN 1773 1835 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1836 1863 S6-OF REPEAT IV (POTENTIAL).
FT DOMAIN 1864 2353 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 520 530 POLY-HIS.
FT DOMAIN 1107 1110 POLY-SER.
FT TRANSMEM 1583 1586 POLY-ARG.
FT SITE 378 378 CALCIUM ION SELECTIVITY AND PERMEABILITY
      (BY SIMILARITY).
FT SITE 974 974 CALCIUM ION SELECTIVITY AND PERMEABILITY
      (BY SIMILARITY).
FT SITE 1504 1504 CALCIUM ION SELECTIVITY AND PERMEABILITY
      (BY SIMILARITY).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1466 1466 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 44 44 F -> S (IN REF. 3).
FT CONFLICT 59 59 C -> G (IN REF. 3).
FT CONFLICT 310 311 DV -> EL (IN REF. 3).
FT CONFLICT 684 684 A -> V (IN REF. 3).
FT CONFLICT 1259 1259 V -> E (IN REF. 3).
FT CONFLICT 1265 1265 R -> W (IN REF. 3).
FT CONFLICT 1563 1563 P -> Q (IN REF. 3).
FT CONFLICT 1609 1609 W -> S (IN REF. 3).
FT CONFLICT 1835 1835 P -> L (IN REF. 3).
FT CONFLICT 1847 1847 L -> A (IN REF. 3).
FT CONFLICT 2218 2218 P -> R (IN REF. 3).
FT SEQUENCE 2353 AA; 259166 MW; 115236748BDC0BD8 CRC64;

Query Match 10.8%; Score 66.5; DB 1; Length 2353;
Best Local Similarity 28.3%; Pred. No. 1.7e+02;
Matches 32; Conservative 12; Mismatches 40; Indels 29; Gaps 5;

QY 9 AILAFSLAQSGAVCKEPEVEVPGGGRKRDPLDQLLQRLFKSHS-SLEGLLKALSOX 67
Db 1977 ASLQIPLAYVSPARSEPLHALSPRG--TARSPSLRLLCRQAEVHTDSLEKIDS----- 2030

QY 68 STDPKSTSPKRDMDHFFVGXMGKRSVQDPSPTDVNQENVPFSGILKYPPRA 120
Db 2031 ---PRDTLDP-----AEPGEKTPVRP--VTQGGSLQSPPRS 2061

RESULT 14
ARPL_CAEEL STANDARD; PRT; 168 AA.
AC Q9N3B0;
AT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE ARP-LIKE PROTEIN PRECURSOR.
GN Y54G2A.O.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE ARP FAMILY.
CC -!- CAUTION: THE ORIGINALLY PREDICTED SEQUENCE WAS INCORRECT AND
CC MERGED TWO DIFFERENT GENES.
CC
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CC EMBL; AC024817; AAF59575.1; ALT_SEQ.
DR WormPep; Y54G2A.O; CE25457.
DR InterPro; IPR000886; BR_target.
KW Hypothetical protein; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 168 ARP-LIKE PROTEIN.
FT SEQUENCE 168 AA; 18968 MW; 5A24379E860A6628 CRC64;

Query Match 10.8%; Score 66; DB 1; Length 168;
Best Local Similarity 21.5%; Pred. No. 10;
Matches 23; Conservative 19; Mismatches 33; Indels 32; Gaps 4;

QY 3 IMLETTAILAFSLAQSGAVCKEPEVEVPGGGRKRDPLDQLLQRLFKSHSLEG 59
Db 5 VLLISLVIVASAAPOCEVCKKLDVDMAKVPAGDSKPD-----AIGKRVIREHC 55

QY 60 LKALSQXSTDPKSTSPKRDMDHFFVGXMGKRSVQDPSPTDVNQE 106
Db 56 -----ETTRNKENKFCFYIGAL-----PESATSIMNE 82

RESULT 15
SDC2_RAT STANDARD; PRT; 201 AA.
AC P34900;
AT 01-FEB-1994 (Rel. 28, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE SYNDSCAN-2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE
DE DE PROTEIN) (HSPG) (SYND2).
GN SDC2 OR SYND2 OR HSPG1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92156130; PubMed=1740437;
RA Pierce A., Lyon M., Hampson I., Cowling G.J., Gallagher J.;
RT "Molecular cloning of the major cell surface heparan sulfate
RT proteoglycan from rat liver.";
RL J. Biol. Chem. 267:3894-3900(1992).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE SYNDSCAN FAMILY OF INTEGRAL MEMBRANE
CC PROTEOGLYCAN.
CC
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CC EMBL; M81687; AAA41355.1; -.
DR PIR; A42261; A42261.
DR InterPro; IPR003585; 4.1m.
DR InterPro; IPR001050; Syndecan.
DR Pfam; PF01034; Syndecan; 1.
DR SMART; SM00294; 4.1m; 1.
DR PROSITE; PS00964; SYNDSCAN; 1.
KW Proteoglycan; Heparan sulfate; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 201 SYNDSCAN-2.
FT DOMAIN 19 144 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 145 169 POTENTIAL.
FT DOMAIN 170 201 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 41 41 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT CARBOHYD 53 53 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT CARBOHYD 55 55 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
```

FT CARBOHYD 57 57 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT SITE 142 143 CLEAVAGE OF ECTODOMAIN (POTENTIAL).
SQ SEQUENCE 201 AA; 22149 MW; 02E08455754C5E5A CRC64;

Query Match 10.8%; Score 66; DB 1; Length 201;
Best Local Similarity 27.6%; Pred. NO. 12;
Matches 21; Conservative 12; Mismatches 41; Indels 2; Gaps 1;

QY 33 GGGRSKRDPDL--YQLLQRLFKSHSLEGLLKALSOXSTDPKSTSPKRDMDHDFVGM 90
Db 58 GAYEDKSPDLTTSQIPRLISLSAAPEVETMTLTKQSTPTQTESPEETDKKEFEISEA 117

QY 91 GKRSVQFDSPTDVNQE 106
Db 118 EEKQDPAVKSTDVYTE 133

Search completed: May 3, 2002, 12:27:21
Job time: 193 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 12:24:28 ; Search time 22.16 Seconds
(without alignments)
798.689 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 613
Sequence: 1 MRIMLLFTAILAFSLAQSGF.....DVNQENVPSFGILKYPPRAE 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL.17.*
1: sp_bacteria.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertibrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	610	99.5	121	4 Q9UHF0	Q9uhf0 homo sapien
2	357.5	58.3	116	11 Q9QXS9	Q9qxs9 mus musculus
3	78.5	12.8	2380	5 Q22896	Q22896 caenorhabdi
4	77	12.6	1008	10 Q9SB51	Q9sb51 arabidopsis
5	77	12.6	1008	10 Q9SPS8	Q9fps8 arabidopsis
6	74.5	12.2	301	5 Q9XV1	Q9xv1 paramocium
7	74	12.1	456	5 Q9V725	Q9v7z5 drosophila
8	72.5	11.8	208	10 Q9FT99	Q9ft99 arabidopsis
9	72.5	11.8	1711	5 Q45409	Q45409 caenorhabdi
10	72	11.7	392	10 Q9SBR6	Q9sbk6 brassica ra
11	71.5	11.7	597	10 Q9FF55	Q9ff55 arabidopsis
12	71	11.6	172	11 Q9D4S8	Q9d4s8 mus musculus
13	71	11.6	605	2 Q9AH41	Q9ah41 neisseria c
14	70.5	11.5	397	2 Q86938	Q86938 streptomyce
15	70	11.4	645	10 Q9FLQ5	Q9flq5 arabidopsis
16	70	11.4	969	2 Q9RZ15	Q9rzi5 deinococcus
17	69.5	11.3	246	3 Q9C239	Q9c239 neurospora
18	69	11.3	309	5 Q9G924	Q9g924 paramocium
19	69	11.3	463	5 Q9VZL5	Q9vzl5 drosophila

20	69	11.3	3076	2 Q9X7E2	Q9x7e2 mycobacteri
21	68.5	11.2	389	5 Q9V9W5	Q9v9w5 drosophila
22	68.5	11.2	962	5 Q9N6U5	Q9n6u5 drosophila
23	68.5	11.2	1006	5 Q9VTE2	Q9vte2 drosophila
24	68	11.1	440	2 Q9KJZ1	Q9kjz1 pseudomonas
25	68	11.1	808	10 Q23052	Q23052 arabidopsis
26	68	11.1	906	10 Q9M2B1	Q9m2b1 arabidopsis
27	67.5	11.0	376	11 Q61048	Q61048 mus musculu
28	67.5	11.0	509	11 Q9D0Q2	Q9d0q2 mus musculu
29	67.5	11.0	578	3 Q9P6V0	Q9p6v0 neurospora
30	67	10.9	229	5 Q9VCJ6	Q9vcj6 drosophila
31	67	10.9	746	6 Q9BE82	Q9be82 macaca fasc
32	66.5	10.8	1536	4 Q9NYI4	Q9nyy4 homo sapien
33	66	10.8	184	4 Q9Y331	Q9y331 homo sapien
34	66	10.8	342	2 Q9RL16	Q9rl16 streptomyce
35	66	10.8	588	13 Q919B3	Q919b3 xenopus lae
36	66	10.8	931	13 Q91995	Q91995 xenopus lae
37	66	10.8	1306	11 Q9JK31	Q9jk31 mus musculu
38	65.5	10.7	134	12 Q85178	Q85178 human parvo
39	65.5	10.7	323	11 Q9EQW6	Q9eqw6 mus musculu
40	65.5	10.7	329	11 Q9JKN4	Q9jkn4 mus musculu
41	65.5	10.7	353	5 Q9NL92	Q9nl92 octopus vul
42	65.5	10.7	839	10 Q9LFE3	Q9lff3 arabidopsis
43	65.5	10.7	1880	5 Q18465	Q18465 hirudo medi
44	65	10.6	227	13 Q9YGT6	Q9ygt6 brachydanio
45	65	10.6	343	3 Q00307	Q00307 bipolaris s

ALIGNMENTS

RESULT 1
Q9UHF0 PRELIMINARY; PRT; 121 AA.
AC Q9UHF0:
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE NEUROKININ B-LIKE PROTEIN ZNEUROK1.
GN ZNEUROK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sheppard P., Jellinek L., Whitmore T., Blumberg H., Lehner J.,
RA O'Hara P.
RT "Homo sapiens homolog of neurokinin B.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=20322570; PubMed=10866201;
RA Page N.M., Woods R.J., Gardiner S.M., Lomthasong K., Gladwell R.T.,
RA Butlin D.J., Manyonda I.T., Lowry P.J.;
RT "Excessive placental neurokinin B secretion during the third trimester
causes pre-eclampsia.";
RL Nature 405:797-800(2000).
DR EMBL; AF186112; AAF01430.1; -;
DR EMBL; AF216586; AAF76980.1; -;
DR InterPro; IPRO02040; Tachykinin.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_1.
SQ SEQUENCE 121 AA; 13438 MW; 14C9AFE2EE9EDECA CRC64;

Query Match 99.5%; Score 610; DB 4; Length 121;
Best Local Similarity 98.3%; Pred. No. 5.7e-60;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRIMLLFTAILAFSLAQSGFCAVCCKPEQEEVPGGSKRDPDLYQLLORLFKSHSLEGL 60
DB 1 MRIMLLFTAILAFSLAQSGFCAVCCKPEQEEVPGGSKRDPDLYQLLORLFKSHSLEGL 60

RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035356; CA23007.1; -
DR EMBL; AL161561; CAB79366.1; -
DR InterPro: IPR001394; UCH-2.
DR InterPro: IPR002893; Znf-MYND.
DR Pfam; PF00442; UCH-1; 1.
DR Pfam; PF00443; UCH-2; 1.
DR Pfam; PF01753; zf-MYND; 1.
DR PROSITE; PS0235; UCH_2_3; 1.
KW Hypothetical protein.
SQ SEQUENCE 1008 AA; 110599 MW; F2DF3BD6E9039B9E CRC64;

Query Match 12.6%; Score 77; DB 10; Length 1008;
Best Local Similarity 33.0%; Pred. No. 7;
Matches 29; Conservative 8; Mismatches 41; Indels 10; Gaps 4;
QY 32 PGGRSRKRDPLVQLQLRPFK-----SHSLEGLLKALSOXSTDPKSTSPKRDHMDFF 86
Db 896 PGGRSGNIOGFSYFQRLKILEEDSASDSSSLFDSNDECSCTDSTSDMD--DFADFI 953
QY 87 VG-XMGKRSVQPD--SPTDVNQENVPF 111
Db 954 FGDRGHRAGGQSTPSPSSSSSSPPF 981

RESULT 5
Q9FPF8 PRELIMINARY; PRT; 1008 AA.
AC Q9FPF8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UBIQUITIN-SPECIFIC PROTEASE 16.
GN UBP16.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20567829; PubMed=11115897;
RA Yan N., Doelling J.H., Falbel T.G., Durski A.M., Vierstra R.D.;
RT "The Ubiquitin-Specific Protease Family from Arabidopsis. AtUBP1 and 2
Are Required for the Resistance to the Amino Acid Analog Canavanine.";
RL Plant Physiol. 124:1828-1843(2000).
DR EMBL; AF302666; AAG42757.1; -
DR InterPro: IPR001394; UCH-2.
DR InterPro: IPR002893; Znf-MYND.
DR Pfam; PF00442; UCH-1; 1.
DR Pfam; PF00443; UCH-2; 1.
DR Pfam; PF01753; zf-MYND; 1.
DR PROSITE; PS0235; UCH_2_3; 1.
KW Protease.
SQ SEQUENCE 1008 AA; 110585 MW; 2BAC6F35ED506DFB CRC64;

Query Match 12.6%; Score 77; DB 10; Length 1008;
Best Local Similarity 33.0%; Pred. No. 7;
Matches 29; Conservative 8; Mismatches 41; Indels 10; Gaps 4;
QY 32 PGGRSRKRDPLVQLQLRPFK-----SHSLEGLLKALSOXSTDPKSTSPKRDHMDFF 86
Db 896 PGGRSGNIOGFSYFQRLKILEEDSASDSSSLFDSNDECSCTDSTSDMD--DFADFI 953
QY 87 VG-XMGKRSVQPD--SPTDVNQENVPF 111
Db 954 FGDRGHRAGGQSTPSPSSSSSSPPF 981

RESULT 6

Q9XYV1 PRELIMINARY; PRT; 301 AA.
AC Q9XYV1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYCLIN-DEPENDENT PROTEIN KINASE CDK2.
GN CDK2.
OS Paramaecium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramaecium.
OX NCBI_TaxID=5888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=51S;
RA Zhang H., Berger J.D.;
RT "A novel member of the cyclin-dependent kinase family in Paramaecium
tetraurelia.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF126147; AAD34354.1; -
DR HSSP; P28523; 1A60.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam; PF00069; pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Cyclin; Kinase; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 301 AA; 34675 MW; E839F1A5EA0D5CB5 CRC64;

Query Match 12.2%; Score 74.5; DB 5; Length 301;
Best Local Similarity 29.3%; Pred. No. 3.2;
Matches 34; Conservative 10; Mismatches 45; Indels 27; Gaps 5;
QY 8 TAILAFSLAQSFGAVCKEPOEEVVP-----GGGRSKRDP-DLYQL-----LQ 48
Db 146 TQIADFGLARAFGLPLKTYTHEVITLWYRAPEILLGQRYSTPVDIWSLGCIFAEMAQR 205
QY 49 RLFSKSHSLEGLLKALSOXSTDPKSTSPKRDHMDFFVCGXMGKRSVQPSPTDVN 104
Db 206 PLFCGSEIDQLPKFKIMGT-PRESTWPGVSTLPDF-----KSTFPRWPTPTN 253

RESULT 7
Q9V7Z5 PRELIMINARY; PRT; 456 AA.
AC Q9V7Z5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CG11395. PROTEIN.
GN CG11395.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Branton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,


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RESULT 10
Q9SBK6
ID Q9SBK6 PRELIMINARY; PRT; 392 AA.
AC Q9SBK6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2001 (TReMBLrel. 16, Last annotation update)
DE FLORAL NECTARY-SPECIFIC PROTEIN.
GN NTRL.
OS Brassica rapa subsp. pekinensis (Chinese cabbage) (Celery cabbage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=51351;
RN [1]
RP SEQUENCE FROM N.A.
RA Song J.T., Seo H.S., Song S.I., Lee J.S., Choi Y.D.;
RT "Characterization of a novel gene expressed specifically in the floral
RT nectarifer of Brassica campestris L. ssp. pekinensis.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF179222; AAF22289.1;
SQ SEQUENCE 392 AA: 43815 MW; 25B78530E93B5757 CRC64;

Query Match 11.7%; Score 72; DB 10; Length 392;
Best Local Similarity 25.7%; Pred. NO. 8.3;
Matches 35; Conservative 18; Mismatches 47; Indels 36; Gaps 8;

QY 10 ILAFLAQSGFVAVCKPEQVEVPGG-----GRSKRPD-----LYQLLQRLFK 52
DB 207 VVALQFQDFVFLRSRSEELVPGRMVLSFLGRSPDPTTESYQWELLAAQLMSLAK 266
QY 53 SHSSLEGLLKALQSXTD-----PKESTSPEKRMHDFVGMXGKRSVQ--PDSPTDVNQE 106
DB 267 -----EGIIE---EENIDAFNAPYAASPEELKM---AIEKSGFSIDRLSPVDWEGG 315
QY 107 NV--PSFGILKYPPRA 120
DB 316 SISDDSYDIVREKPEA 331

RESULT 11
Q9FF55
ID Q9FF55 PRELIMINARY; PRT; 597 AA.
AC Q9FF55;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE PROTEIN DISULPHIDE ISOMERASE-LIKE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=COLUMBIA;
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyaajina N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT pl clones.";
RL DNA Res. 4:215-230(1997).
DR EMBL; AB005246; BAB09837.1;
DR InterPro; IPR000886; ER.target.
DR InterPro; IPR000063; ThioRed.
DR Pfam; PF00085; thioRed; 3.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Isomerase.
SQ SEQUENCE 597 AA: 66357 MW; 5A8FC7E72AA64B2B CRC64;
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Query Match 11.7%; Score 71.5; DB 10; Length 597;
Best Local Similarity 24.8%; Pred. No. 15;
Matches 27; Conservative 17; Mismatches 30; Indels 35; Gaps 5;

QY 2 RIMLFL--TAILAFS-LAQSGA-----VKPEQVEVPGG----- 34
DB 4 RVLLFLSLTALLFSAVSPFAASSDDVDRLSLFLEDLKEDDVPAGADSLSSSTGTFDEF 63
QY 35 -GRSKRPDLYQLLQRLFKSHSSLSGLLKALQSXTDPKESTSPKRD 82
DB 64 EGGEEDPMY-----NDDDEEGFSDUGNPDSDPLPTPEIDKDV 105

RESULT 12
Q9D4S8
ID Q9D4S8 PRELIMINARY; PRT; 172 AA.
AC Q9D4S8;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE 4930563P03RIK PROTEIN.
GN 4930563P03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Sato T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK016213; BAB30150.1;
DR MGD; MGI:1914905; 4930563P03RIK.
SQ SEQUENCE 172 AA: 19043 MW; E3243D9122FC5811 CRC64;
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Query Match 11.6%; Score 71; DB 11; Length 172;
Best Local Similarity 26.4%; Pred. No. 4;
Matches 32; Conservative 16; Mismatches 55; Indels 18; Gaps 6;

QY 2 RIMLFTAILAFSLAQSGFVAVCKPEQVEVPGGSKRDPDLYQLLQRLFKSHSSLEGIL 61
DB 3 RIILVVAVQPHQ-QQMFGEELPESQDGEQPGPARKKQPSMSEAMPLYTLCKEDLESMD 61
QY 62 K----ALSOXSTDPR-ESTSPKRDMDHDFVGMXMKRSVQDPS--TDVNQE---NVPSF 111
DB 62 KEVDILGEGSDSDIETKKKPEDQNEQ-----ERAPKPKRPAPGIRREQVGLPSS 114
QY 112 G 112
DB 115 G 115
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 12:24:48 ; Search time 24 Seconds
(without alignments)
373.453 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 121
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Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 0

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119	98.3	121	19 AAW75228	Human secreted pro
2	66	54.5	121	19 AAW75212	Human secreted pro
3	66	54.5	121	20 AAW97213	A human zneurokl p
4	66	54.5	121	20 AAW74413	HPMB091 protein se
5	66	54.5	121	22 AAW82380	Human neurokinin B
6	66	54.5	122	20 AAW96144	Human preprotachy
7	66	54.5	135	21 AAW33445	Human PRO1155 prot
8	66	54.5	135	21 AAW66739	Membrane-bound pro
9	66	54.5	135	22 AAW65262	Human PRO1155 (UNQ
10	49	40.5	51	20 AAY12634	Human 5' EST secre
11	27	22.3	39	20 AAW74414	HPMB091 protein se

Fragment of human	36	19	AAW75249	19.0	23	12
Fragment of human	15	19	AAW75250	8.3	10	13
A murine homologue	92	20	AAW97214	8.3	10	14
Rat preprotachykin	116	20	AAW96146	8.3	10	15
Bovine preprotachy	126	20	AAW96145	8.3	10	16
Decapeptide for tr	10	5	AAW40414	6.6	10	17
Neurokinin B. Syn	10	16	AAW77312	6.6	8	18
Fragment of human	10	19	AAW75251	6.6	8	19
Neurokinin B. Mam	10	19	AAW79777	6.6	8	20
Protein binding po	10	20	AAW23264	6.6	8	21
Human tachykinin a	10	20	AAW92697	6.6	8	22
HPMB091 protein se	10	20	AAW74415	6.6	8	23
Human tachykinin a	10	20	AAW92728	6.6	8	24
Neurokinin B pepti	10	22	AAW99356	6.6	8	25
Neurokinin B pepti	10	22	AAW99352	6.6	8	26
Human neurokinin B	10	22	AAW82381	6.6	8	27
Tachykinins peptid	10	22	AAW91368	6.6	8	28
Tachykinins peptid	10	22	AAW91397	6.6	8	29
Tachykinins peptid	11	22	AAW91371	6.6	8	30
Arabidopsis thalia	209	21	AAW20184	5.8	7	31
Human protein sequ	507	22	AAW92617	5.8	7	32
Amino acid sequenc	590	22	AAW84261	5.8	7	33
Grk5-green floures	836	19	AAW85017	5.8	7	34
Grk5-green floures	842	19	AAW85008	5.8	7	35
Human polypeptide	913	22	AAW41078	5.8	7	36
Micromonospora eve	1145	22	AAU04895	5.8	7	37
Tachykinins peptid	9	22	AAW91369	5.0	6	38
Human tachykinin a	10	20	AAW92698	5.0	6	39
Tachykinins peptid	10	22	AAW91370	5.0	6	40
Human secreted pro	20	21	AAW56361	5.0	6	41
Signal peptide for	25	11	AAW07569	5.0	6	42
Compact structure	26	20	AAW49762	5.0	6	43
GRK6 palmitoylatio	26	21	AAW88078	5.0	6	44
Palmitoylation seq	26	21	AAW43822	5.0	6	45
Transdominant effe	26	22	AAW45937	5.0	6	46
Myristylation sequ	26	22	AAW35069	5.0	6	47
HIV-1 non-subtype	29	21	AAW69224	5.0	6	48
Signal peptide for	33	11	AAW07570	5.0	6	49
Peptide #4647 enco	36	22	AAW18213	5.0	6	50
Peptide #4744 enco	36	22	AAW30707	5.0	6	51
Haem protein relat	41	22	AAW04661	5.0	6	52
Arabidopsis thalia	43	21	AAW45989	5.0	6	53
Hepatitis C virus	48	17	AAW96536	5.0	6	54
Human foetal prote	50	22	AAW06574	5.0	6	55
Human hypoxia indu	63	20	AAW42136	5.0	6	56
Human gene 60 enco	63	22	AAW06100	5.0	6	57
Human secreted pro	64	21	AAW00286	5.0	6	58
Human secreted pro	64	22	AAW64957	5.0	6	59
Peptide #2 associa	70	21	AAW45282	5.0	6	60
Human secreted pro	75	21	AAW03127	5.0	6	61
Human prostate tum	78	20	AAW73973	5.0	6	62
Arabidopsis thalia	82	21	AAW33806	5.0	6	63
Human prostate can	85	21	AAW56505	5.0	6	64
Arabidopsis thalia	86	21	AAW17328	5.0	6	65
Human 5' EST relat	88	21	AAW65405	5.0	6	66
Human 5' EST secre	92	20	AAW11677	5.0	6	67
Gene 11 human secr	93	21	AAW51890	5.0	6	68
Cysteine protease	96	22	AAW65783	5.0	6	69
Ferric enterobacti	98	18	AAW28296	5.0	6	70
Protein encoded by	104	21	AAW94765	5.0	6	71
Human colon cancer	105	22	AAW77654	5.0	6	72
Rac2-related prote	106	21	AAW33907	5.0	6	73
Human secreted pro	110	22	AAW65745	5.0	6	74
Human protein sequ	111	22	AAW93534	5.0	6	75
Human secreted pro	112	21	AAW00737	5.0	6	76
Peptide #10025 enc	114	22	AAW35988	5.0	6	77
S. pneumoniae argi	116	19	AAW38606	5.0	6	78
S. aureus polypept	118	20	AAW03786	5.0	6	79
Human secreted pro	118	21	AAW03906	5.0	6	80
Human secreted pro	122	22	AAW87212	5.0	6	81
Human gene 60 enco	122	22	AAW06194	5.0	6	82
Amino acid sequenc	125	20	AAW29204	5.0	6	83
						84

85	6	5.0	127	21	AAB32666	Eucalyptus grandis	158	222	22	AAB61778	Sunflower pathogen
86	6	5.0	129	19	AAW69949	DN722_2 protein.	159	223	21	AAV44260	Asparagus officina
87	6	5.0	135	21	AAV95852	Autoantigen diagno	160	223	21	AAH61784	Sunflower pathogen
88	6	5.0	136	22	AAH65744	Rac2-related prote	161	224	21	AAV57749	Arabidopsis thalia
89	6	5.0	139	18	AAW23003	Canine herpesvirus	162	224	21	AAV59664	Secreted protein 1
90	6	5.0	139	19	AAW72663	Canine herpes viru	163	225	20	AAV42441	Cytokine family me
91	6	5.0	139	22	AAH51120	Canine herpes viru	164	225	20	AAW85731	z219a polypeptide
92	6	5.0	144	21	AAH59087	Breast and ovarian	165	225	20	AAV17835	Human PRO365 prote
93	6	5.0	145	19	AAW38463	Mouse RNA-binding	166	225	21	AAH25762	Human PRO365 polyp
94	6	5.0	146	21	AAW45988	Arabidopsis thalia	167	225	21	AAH01326	Human secreted pro
95	6	5.0	149	22	AAH99856	Physcomitrella pat	168	225	22	AAU12366	Human PRO365 polyp
96	6	5.0	153	20	AAW29391	Sperm whale myoglo	169	225	22	AAU14503	Human novel protei
97	6	5.0	153	20	AAW81769	Whale MYGL peptide	170	225	22	AAH85208	Human 2-21 protein
98	6	5.0	153	21	AAV69975	MYGL protein. Uni	171	225	22	AAH01045	Human secreted tum
99	6	5.0	154	21	AAW47234	Arabidopsis thalia	172	225	22	AAH31188	Amino acid sequenc
100	6	5.0	157	20	AAV31806	Beak and feather d	173	225	22	AAH75348	Secreted protein #
101	6	5.0	157	21	AAV81598	Streptococcus pneu	174	225	21	AAV79197	Human diarylsulfon
102	6	5.0	158	21	AAW47233	Arabidopsis thalia	175	225	20	AAH85732	z219a polypeptide
103	6	5.0	160	21	AAW53452	Arabidopsis thalia	176	225	20	AAH52374	Escherichia coli F
104	6	5.0	161	21	AAW12312	Zea mays protein f	177	225	22	AAW41883	Human polypeptide
105	6	5.0	161	22	AAH95034	Human protein sequ	178	225	22	AAH03787	Human gene 1 encod
106	6	5.0	164	20	AAV03791	S. aureus polyypept	179	225	21	AAH57748	Arabidopsis thalia
107	6	5.0	166	21	AAH56356	Human secreted pro	180	225	22	AAH01059	Human secreted tum
108	6	5.0	166	22	AAH18394	Peptide #4828 enco	181	225	22	AAH94584	Human protein sequ
109	6	5.0	174	21	AAH41067	Human ORFX ORF831	182	229	20	AAV45335	Human secreted pro
110	6	5.0	175	18	AAW28333	Staphylococcus aur	183	229	19	AAW72933	Mycobacterium tube
111	6	5.0	175	21	AAH11131	Arabidopsis thalia	184	225	20	AAV21953	Amino acid sequenc
112	6	5.0	175	21	AAH51901	Arabidopsis thalia	185	225	20	AAW56334	Homo sapiens secre
113	6	5.0	177	15	AAH60895	Borrelia J1 antige	186	225	22	AAW24121	Human EST encoded
114	6	5.0	177	15	AAH62781	Borrelia J1 antige	187	225	22	AAH38873	Human polypeptide
115	6	5.0	177	15	AAH62782	Borrelia J1 antige	188	225	22	AAH27243	Human polypeptide
116	6	5.0	177	17	AAH83037	Partial transposas	189	225	20	AAV29128	Amino acid sequenc
117	6	5.0	180	21	AAH28680	Arabidopsis thalia	190	225	20	AAV03752	S. aureus Ferrichr
118	6	5.0	183	20	AAV36865	Protein involved i	191	225	22	AAH82441	S. epidermidis ope
119	6	5.0	183	22	AAH65707	Novel protein kina	192	225	22	AAH71376	Human secreted pro
120	6	5.0	184	19	AAH38464	Mouse RNA-binding	193	225	22	AAH40659	Human polypeptide
121	6	5.0	187	21	AAH51842	Arabidopsis thalia	194	225	22	AAU01003	Human EXMAD-21 SEQ
122	6	5.0	187	22	AAU14267	Human novel protei	195	225	18	AAW37354	Amino acid sequenc
123	6	5.0	187	22	AAH91067	C glutamicum prote	196	225	21	AAV74966	Neisseria gonorrhoe
124	6	5.0	187	22	AAH80020	Corynebacterium gl	197	225	22	AAH90549	C glutamicum prote
125	6	5.0	190	21	AAH07286	Arabidopsis thalia	198	225	20	AAV49440	S. typhimurium ary
126	6	5.0	190	21	AAH09587	Arabidopsis thalia	199	225	20	AAH11686	A. vitis hypersens
127	6	5.0	190	21	AAH10859	Arabidopsis thalia	200	225	21	AAH44770	Soybean serine O-a
128	6	5.0	190	21	AAH37456	Arabidopsis thalia	201	225	20	AAW78467	Thermus species sp
129	6	5.0	191	21	AAH29836	Arabidopsis thalia	202	225	20	AAW78468	T. filiformis DNA p
130	6	5.0	193	22	AAH85210	Arabidopsis thalia	203	225	20	AAW78463	T. flavus DNA polym
131	6	5.0	194	15	AAH60896	Borrelia J1 antige	204	225	22	AAH91709	C glutamicum prote
132	6	5.0	196	21	AAH11130	Arabidopsis thalia	205	225	20	AAH78462	T. aquaticus DNA po
133	6	5.0	196	21	AAH51900	Arabidopsis thalia	206	225	21	AAH56653	Human prostate can
134	6	5.0	197	21	AAH07396	Arabidopsis thalia	207	225	21	AAH76748	Human protein kina
135	6	5.0	197	21	AAH30192	Arabidopsis thalia	208	225	22	AAH06206	Human protein kina
136	6	5.0	197	21	AAH32599	Arabidopsis thalia	209	225	22	AAH92549	C glutamicum prote
137	6	5.0	197	21	AAH48944	Arabidopsis thalia	210	225	22	AAH81198	Human RNA-binding
138	6	5.0	197	21	AAH33999	Arabidopsis thalia	211	225	22	AAH46733	T. aquaticus DNA p
139	6	5.0	198	21	AAH42941	Human ORFX ORF2705	212	225	17	AAH96265	Mutant Thermus aqu
140	6	5.0	199	21	AAH29835	Arabidopsis thalia	213	225	17	AAH96265	Arabidopsis thalia
141	6	5.0	199	21	AAH31741	Arabidopsis thalia	214	225	21	AAH39465	Arabidopsis thalia
142	6	5.0	200	21	AAH28679	Arabidopsis thalia	215	225	21	AAH93902	Amino acid sequenc
143	6	5.0	204	20	AAH34533	Porphomonas ging	216	225	21	AAH71117	Human Hydrolase pr
144	6	5.0	205	21	AAH48044	Arabidopsis thalia	217	225	17	AAH96268	Mutant Thermus aqu
145	6	5.0	206	22	AAH85209	22.8 kDa human 2-2	218	225	18	AAW24210	Cleavage BN/thromb
146	6	5.0	208	21	AAH51841	Arabidopsis thalia	219	225	19	AAH79955	Cleavage BN/thromb
147	6	5.0	208	21	AAV75093	Neisseria gonorrhoe	220	225	19	AAH59937	Amino acid sequenc
148	6	5.0	208	21	AAH75094	Neisseria meningit	221	225	17	AAH96266	Thermus aquaticus
149	6	5.0	211	22	AAH62722	B. garinii ospC pro	222	225	32	AAH72129	Human olfactory re
150	6	5.0	212	12	AAH13140	B. burgdorferi stra	223	225	6	AAH72532	Human OR-like poly
151	6	5.0	212	16	AAH75729	B. burgdorferi str	224	225	33	AAH93767	Human protein sequ
152	6	5.0	212	18	AAW41624	B. afzeiili Ospc.	225	225	21	AAH95335	Human quaking spli
153	6	5.0	212	22	AAW40188	Human polypeptide	226	225	22	AAH92318	C glutamicum prote
154	6	5.0	219	21	AAH07285	Arabidopsis thalia	227	225	22	AAH06086	Human gene 46 enco
155	6	5.0	219	21	AAH09586	Arabidopsis thalia	228	225	32	AAH08544	Mesothelin related
156	6	5.0	219	21	AAH37455	Arabidopsis thalia	229	225	38	AAH87109	Human secreted pro
157	6	5.0	221	20	AAH34400	Porphomonas ging	230	225	21	AAH36232	Arabidopsis thalia

231	6	5.0	330	22	AAG92260	C glutamicum prote	304	6	5.0	459	19	AAW38457	Human RNA-binding
232	6	5.0	332	22	AAG92055	C glutamicum prote	305	6	5.0	463	22	AAW71254	Human gene 12-enco
233	6	5.0	333	22	AAW42076	Human polypeptide	306	6	5.0	465	21	AAW83150	NGSP polypeptide o
234	6	5.0	337	22	AAW12503	Human MATH-2 prote	307	6	5.0	467	21	AAW88483	Human membrane or
235	6	5.0	337	22	AAW60352	Mouse atonal homol	308	6	5.0	470	22	AAW40522	Human polypeptide
236	6	5.0	337	22	AAW60368	Mouse atonal homol	309	6	5.0	470	22	AAW40523	Human polypeptide
237	6	5.0	341	21	AAW95336	Human quaking spli	310	6	5.0	475	21	AAW70414	Neisseria meningit
238	6	5.0	342	20	AAW07862	Human secreted pro	311	6	5.0	478	22	AAW20314	Soybean apoptosis
239	6	5.0	344	14	AAW40918	Bacillus subtilis	312	6	5.0	482	18	AAW06540	C5a-like seven tra
240	6	5.0	348	17	AAW01619	Human uridine diph	313	6	5.0	483	19	AAW37064	HIV-1 breakthrough
241	6	5.0	348	22	AAW54118	Amino acid sequenc	314	6	5.0	483	21	AAW18325	Arabidopsis thalia
242	6	5.0	354	21	AAW51152	Human UDP galactos	315	6	5.0	483	21	AAW46788	Arabidopsis thalia
243	6	5.0	354	21	AAW36231	Arabidopsis thalia	316	6	5.0	484	8	AAW70458	Sequence of gpd en
244	6	5.0	356	22	AAW92897	C glutamicum prote	317	6	5.0	486	22	AAW33541	Human protein sequ
245	6	5.0	358	21	AAW04826	Arabidopsis thalia	318	6	5.0	487	19	AAW37065	HIV-1 breakthrough
246	6	5.0	358	21	AAW61479	Arabidopsis thalia	319	6	5.0	489	22	AAW71293	Human gene 12-enco
247	6	5.0	363	22	AAW03764	Arabidopsis thalia	320	6	5.0	491	16	AAW72369	Human auxillary cy
248	6	5.0	368	22	AAW76567	Human gene 1 encod	321	6	5.0	491	17	AAW83176	Human cytochrome p
249	6	5.0	370	21	AAW52996	Corynebacterium g1	322	6	5.0	491	17	AAW81468	Human derived cyto
250	6	5.0	371	20	AAW95171	Neisseria meningit	323	6	5.0	498	21	AAW70413	Neisseria meningit
251	6	5.0	374	13	AAW25049	Protein exhibiting	324	6	5.0	499	21	AAW75748	Neisseria gonorrhe
252	6	5.0	375	19	AAW98466	H. pylori GHP0 782	325	6	5.0	499	21	AAW75749	Neisseria meningit
253	6	5.0	376	21	AAW36230	Arabidopsis thalia	326	6	5.0	499	21	AAW75750	Neisseria meningit
254	6	5.0	377	19	AAW70902	Human cytochrome P	327	6	5.0	499	21	AAW52993	Neisseria meningit
255	6	5.0	380	22	AAW80034	Corynebacterium g1	328	6	5.0	499	21	AAW52994	Neisseria meningit
256	6	5.0	381	20	AAW81821	Human secreted pro	329	6	5.0	502	21	AAW53884	Neisseria meningit
257	6	5.0	381	20	AAW55787	Human ZIRI protein	330	6	5.0	502	21	AAW53884	Arabidopsis thalia
258	6	5.0	386	22	AAW62727	Human zinc RING (2	331	6	5.0	504	21	AAW16593	Arabidopsis thalia
259	6	5.0	390	20	AAW42325	Borrelia sp chim	332	6	5.0	511	9	AAW81161	Recombinant alpha-
260	6	5.0	390	20	AAW17496	Human Toso protein	333	6	5.0	511	9	AAW81180	Sequence of alpha-
261	6	5.0	392	21	AAW05001	Human Toso protein	334	6	5.0	512	11	AAW07574	Chitinase derivati
262	6	5.0	402	21	AAW77276	Human PIGRL-1 prot	335	6	5.0	512	15	AAW48670	N. crassa cellobio
263	6	5.0	402	21	AAW08547	Arabidopsis thalia	336	6	5.0	516	16	AAW80279	Human protease and
264	6	5.0	393	21	AAW54097	Human PIGRL-1 prot	337	6	5.0	516	16	AAW80279	Mutant Thermus aqu
265	6	5.0	399	21	AAW08543	Human pancreatic c	338	6	5.0	517	22	AAW74679	Arabidopsis thalia
266	6	5.0	402	21	AAW08547	Mesothelin related	339	6	5.0	528	17	AAW96267	Arabidopsis thalia
267	6	5.0	402	21	AAW77276	Soluble mesothelin	340	6	5.0	532	21	AAW39876	Heat shock protein
268	6	5.0	402	21	AAW78828	Streptomyces cinn	341	6	5.0	532	21	AAW39876	Arabidopsis thalia
269	6	5.0	403	21	AAW42261	Amino acid sequenc	342	6	5.0	537	21	AAW14498	Arabidopsis thalia
270	6	5.0	404	21	AAW81196	Human secreted pro	343	6	5.0	541	19	AAW77406	Arabidopsis thalia
271	6	5.0	404	21	AAW81196	Human gene 46 enco	344	6	5.0	547	21	AAW39875	Arabidopsis thalia
272	6	5.0	410	22	AAW06173	Borrelia sp chim	345	6	5.0	547	22	AAW69060	Arabidopsis thalia
273	6	5.0	414	21	AAW04825	Arabidopsis thalia	346	6	5.0	548	17	AAW96263	Pseudomonas aerugi
274	6	5.0	414	21	AAW53885	Arabidopsis thalia	347	6	5.0	548	21	AAW22282	Mutant Thermus aqu
275	6	5.0	414	21	AAW61478	Arabidopsis thalia	348	6	5.0	549	21	AAW14497	Arabidopsis thalia
276	6	5.0	415	21	AAW83151	NGSP polypeptide o	349	6	5.0	551	20	AAW23907	Arabidopsis thalia
277	6	5.0	415	21	AAW04824	Arabidopsis thalia	350	6	5.0	551	20	AAW23907	Amino acid sequenc
278	6	5.0	415	21	AAW61477	Arabidopsis thalia	351	6	5.0	556	16	AAW79586	S. cerevisiae esse
279	6	5.0	428	21	AAW16594	Arabidopsis thalia	352	6	5.0	557	21	AAW53140	Mouse TCP-1 subuni
280	6	5.0	429	20	AAW27406	Arabidopsis thalia	353	6	5.0	557	21	AAW33140	Macaca mulatta rha
281	6	5.0	429	21	AAW80086	Human cytochrome P	354	6	5.0	560	22	AAW62724	Borrelia sp chim
282	6	5.0	430	21	AAW22042	Citrate transport	355	6	5.0	560	22	AAW56476	Amino acid sequenc
283	6	5.0	431	20	AAW42295	Arabidopsis thalia	356	6	5.0	562	22	AAW62100	Human bridging int
284	6	5.0	439	18	AAW23447	Human cytochrome P	357	6	5.0	565	21	AAW70011	Human protease and
285	6	5.0	439	18	AAW23449	Pseudomonas putida	358	6	5.0	565	21	AAW32435	Human ubiquitin sp
286	6	5.0	439	18	AAW23449	Pseudomonas putida	359	6	5.0	570	21	AAW19444	Human chaperone pr
287	6	5.0	439	18	AAW23450	Pseudomonas putida	360	6	5.0	570	21	AAW19444	Human secreted pro
288	6	5.0	439	18	AAW23453	Pseudomonas putida	361	6	5.0	574	22	AAW69061	pTcHisB expressio
289	6	5.0	439	19	AAW23454	Pseudomonas putida	362	6	5.0	576	16	AAW71375	Rat GRK encoded by
290	6	5.0	439	19	AAW38466	Mouse RNA-binding	363	6	5.0	576	16	AAW71374	Human GRK #2. Hom
291	6	5.0	441	21	AAW14499	Arabidopsis thalia	364	6	5.0	576	20	AAW23925	Amino acid sequenc
292	6	5.0	441	21	AAW22041	Arabidopsis thalia	365	6	5.0	576	22	AAW73349	HTM clone 1253545
293	6	5.0	442	18	AAW23448	Pseudomonas putida	366	6	5.0	576	22	AAW84262	Amino acid sequenc
294	6	5.0	442	18	AAW23456	Pseudomonas putida	367	6	5.0	579	22	AAW84527	Human protein sequ
295	6	5.0	444	18	AAW23455	Pseudomonas putida	368	6	5.0	581	22	AAW59832	TutI protein. Tha
296	6	5.0	448	21	AAW70409	Neisseria meningit	369	6	5.0	594	21	AAW16592	Arabidopsis thalia
297	6	5.0	449	21	AAW43854	Human cancer assoc	370	6	5.0	594	21	AAW53883	Arabidopsis thalia
298	6	5.0	452	18	AAW23452	Pseudomonas putida	371	6	5.0	601	21	AAW79240	Human diarylsulfon
299	6	5.0	453	21	AAW43841	Human cancer assoc	372	6	5.0	609	20	AAW37619	Amino acid sequenc
300	6	5.0	454	20	AAW06921	Human ZIP-kinase (373	6	5.0	611	22	AAW85021	Shrimp white spot
301	6	5.0	454	22	AAW94378	Human protein sequ	374	6	5.0	622	15	AAW53992	Megakaryocyte pote
302	6	5.0	455	22	AAW68328	Amino acid sequenc	375	6	5.0	632	18	AAW26674	Human CAK1 antigen
303	6	5.0	459	18	AAW23451	Pseudomonas putida	376	6	5.0	633	21	AAW71373	Human GRK #1. Hom
	6	5.0	459	19	AAW38454	Mouse RNA-binding						AAW31402	Arabidopsis thalia

377	6	5.0	650	21	AAB42495	Human ORFX ORF2259	450	6	5.0	888	22	AAW40290	Human polypeptide
378	6	5.0	654	22	AAB95459	Human protein sequ	451	6	5.0	889	20	AAW24913	Human ontherin. H
379	6	5.0	672	22	AAB93091	Human protein sequ	452	6	5.0	889	20	AAW21687	Cadherin-like poly
380	6	5.0	686	21	AAG31101	Arabidopsis thalia	453	6	5.0	908	20	AAV33450	Chimeric taq DNA p
381	6	5.0	695	17	AAR96264	Mutant Thermus aqu	454	6	5.0	908	20	AAV33451	Chimeric taq DNA p
382	6	5.0	720	22	AAW72081	Nicotiana tabacum	455	6	5.0	910	20	AAV33448	Chimeric taq DNA p
383	6	5.0	737	16	AAR76640	Deltex protein. H	456	6	5.0	910	20	AAV33449	Chimeric taq DNA p
384	6	5.0	737	16	AAR76639	Deltex protein pro	457	6	5.0	931	16	AAW79009	Human DNA repair p
385	6	5.0	737	18	AAW18317	Drosophila Deltex	458	6	5.0	941	22	AAW04778	Human vesicle traf
386	6	5.0	738	22	AAW32927	Human polypeptide	459	6	5.0	948	17	AAW53332	Tumor necrosis fac
387	6	5.0	745	22	AAW41083	Human polypeptide	460	6	5.0	948	18	AAW35375	TNF-R1-DD ligand p
388	6	5.0	748	22	AAW40225	Human polypeptide	461	6	5.0	949	20	AAV33452	Chimeric taq DNA p
389	6	5.0	757	13	AAW23141	Mutant thermostabl	462	6	5.0	982	20	AAV33453	Chimeric taq DNA p
390	6	5.0	758	13	AAW23154	Mutant thermostabl	463	6	5.0	1029	21	AAW24027	Human PRO3434 prot
391	6	5.0	783	21	AAV75533	Neisseria meningit	464	6	5.0	1029	21	AAV96736	PRO3434, a novel s
392	6	5.0	783	21	AAV75534	Neisseria meningit	465	6	5.0	1054	22	AAW68897	Human HX2004-6 pro
393	6	5.0	787	13	AAW23142	Mutant thermostabl	466	6	5.0	1054	22	AAW68898	Human HX2004-6 pro
394	6	5.0	788	13	AAW23153	Mutant thermostabl	467	6	5.0	1077	22	AAU01924	Human adenylyase cy
395	6	5.0	797	21	AAB40601	Human ORFX ORF365	468	6	5.0	1141	22	AAW85008	Shrimp white spot
396	6	5.0	810	22	AAB62314	T. aquaticus (Taq)	469	6	5.0	1156	21	AAB10104	Feline foamy virus
397	6	5.0	823	17	AAW00364	Human CDC27. Homo	470	6	5.0	1221	20	AAV05940	Thermophilus therm
398	6	5.0	823	19	AAW98507	H. pylori GHPO 122	471	6	5.0	1255	20	AAV05944	Thermophilus therm
399	6	5.0	824	16	AAW75848	H-NOC retinoblasto	472	6	5.0	1272	21	AAV70596	Rat multidrug resi
400	6	5.0	830	13	AAW23152	Mutant thermostabl	473	6	5.0	1272	21	AAV70597	Rat multidrug resi
401	6	5.0	830	16	AAR76060	Tfifl DNA-polymeras	474	6	5.0	1275	21	AAV78879	Rat mdrlb2 multidr
402	6	5.0	831	16	AAR64273	T. flavus DNA-poly	475	6	5.0	1275	22	AAW60409	P. chrysogenum ABC
403	6	5.0	831	19	AAW79961	Thermus flavus DNA	476	6	5.0	1297	22	AAB62491	Human protein sequ
404	6	5.0	831	20	AAW80428	DNA polymerase enz	477	6	5.0	1504	22	AAW95729	Murine APC-2 polyp
405	6	5.0	832	10	AAW90556	Purified native th	478	6	5.0	1674	21	AAV92060	Novel protein kin
406	6	5.0	832	13	AAW23140	Mutant thermostabl	479	6	5.0	1920	22	AAW65856	Novel APC-2 protei
407	6	5.0	832	13	AAW22602	Taq polymerase enc	480	6	5.0	2274	22	AAW50674	Mouse APC-2 protei
408	6	5.0	832	13	AAW22603	Taq polymerase enc	481	6	5.0	4473	17	AAW97244	Virulence gene clu
409	6	5.0	832	13	AAW22604	Taq polymerase enc	482	6	5.0	7257	17	AAW85876	Sorangium cellulos
410	6	5.0	832	16	AAW76690	Taq DNA-polymerase	483	6	5.0	1674	21	AAW87912	Peptide antagonisi
411	6	5.0	832	16	AAW76691	DNA-polymerase REM	484	6	5.0	1674	21	AAW87912	Hepatitis C virus
412	6	5.0	832	16	AAW76692	DNA-polymerase REM	485	6	5.0	1674	21	AAW87912	Peptide encoded by
413	6	5.0	832	16	AAW76693	DNA-polymerase (F7	486	6	5.0	1674	21	AAW87912	Amino acid probe f
414	6	5.0	832	16	AAW64272	T. aquaticus DNA-p	487	6	5.0	1674	21	AAW87912	B. thuringiensis e
415	6	5.0	832	19	AAW79960	Thermus aquaticus	488	6	5.0	1674	21	AAW87912	Tumour homing pep
416	6	5.0	832	19	AAW79963	Thermus DNA polyme	489	6	5.0	1674	21	AAW87912	Human breast cance
417	6	5.0	832	19	AAW76209	T. aquaticus DNA p	490	6	5.0	1674	21	AAW87912	Human breast tumou
418	6	5.0	832	19	AAW76210	T. aquaticus DNA p	491	6	5.0	1674	21	AAW87912	Peptide #2 used in
419	6	5.0	832	19	AAW76211	T. aquaticus DNA p	492	6	5.0	1674	21	AAW87912	Peptide probe #2.
420	6	5.0	832	19	AAW76208	T. aquaticus DNA p	493	6	5.0	1674	21	AAW87912	HBV pol 541 peptid
421	6	5.0	832	19	AAW76203	T. aquaticus DNA p	494	6	5.0	1674	21	AAW87912	Alternative ORF3 e
422	6	5.0	832	19	AAW76204	T. aquaticus DNA p	495	6	5.0	1674	21	AAW87912	Hepatitis B virus
423	6	5.0	832	19	AAW76205	T. aquaticus DNA p	496	6	5.0	1674	21	AAW87912	Tumour antigen pep
424	6	5.0	832	19	AAW76206	T. aquaticus DNA p	497	6	5.0	1674	21	AAW87912	Peptide fragment o
425	6	5.0	832	19	AAW76207	T. aquaticus DNA p	498	6	5.0	1674	21	AAW87912	Fragment of namato
426	6	5.0	832	19	AAW61087	Taq DNA polymerase	499	6	5.0	1674	21	AAW87912	LXXLL signature mo
427	6	5.0	832	19	AAW61088	Taq DNA polymerase	500	6	5.0	1674	21	AAW87912	Human complementar
428	6	5.0	832	19	AAW61089	Taq DNA polymerase	501	6	5.0	1674	21	AAW87912	Human complementar
429	6	5.0	832	19	AAW61090	Taq DNA polymerase	502	6	5.0	1674	21	AAW87912	Human complementar
430	6	5.0	832	19	AAW61091	Taq DNA polymerase	503	6	5.0	1674	21	AAW87912	Human complementar
431	6	5.0	832	19	AAW61092	Taq DNA polymerase	504	6	5.0	1674	21	AAW87912	Human complementar
432	6	5.0	832	19	AAW23962	Modified taq polym	505	6	5.0	1674	21	AAW87912	Human complementar
433	6	5.0	832	19	AAW60427	DNA polymerase enz	506	6	5.0	1674	21	AAW87912	Human complementar
434	6	5.0	832	22	AAW67547	Amino acid sequenc	507	6	5.0	1674	21	AAW87912	Human complementar
435	6	5.0	832	22	AAW67549	Amino acid sequenc	508	6	5.0	1674	21	AAW87912	Human complementar
436	6	5.0	833	16	AAW64275	DNA-polymerase con	509	6	5.0	1674	21	AAW87912	Human complementar
437	6	5.0	833	17	AAW96262	Mutant Thermus aqu	510	6	5.0	1674	21	AAW87912	Human complementar
438	6	5.0	833	18	AAW24211	Cleavage DN nuclea	511	6	5.0	1674	21	AAW87912	Human complementar
439	6	5.0	833	18	AAW24212	Cleavage DA nuclea	512	6	5.0	1674	21	AAW87912	Human complementar
440	6	5.0	833	18	AAW24213	Cleavage DV nuclea	513	6	5.0	1674	21	AAW87912	Human complementar
441	6	5.0	833	19	AAW79966	Cleavage DN nuclea	514	6	5.0	1674	21	AAW87912	Human complementar
442	6	5.0	833	19	AAW79967	Cleavage DA nuclea	515	6	5.0	1674	21	AAW87912	Human complementar
443	6	5.0	833	19	AAW79968	Cleavage DV nuclea	516	6	5.0	1674	21	AAW87912	Human complementar
444	6	5.0	833	19	AAW59941	Amino acid sequenc	517	6	5.0	1674	21	AAW87912	Human complementar
445	6	5.0	833	19	AAW59938	Amino acid sequenc	518	6	5.0	1674	21	AAW87912	Human complementar
446	6	5.0	833	19	AAW59942	Amino acid sequenc	519	6	5.0	1674	21	AAW87912	Human complementar
447	6	5.0	833	20	AAW80430	Consensus sequence	520	6	5.0	1674	21	AAW87912	Human complementar
448	6	5.0	845	16	AAW72875	Tsps17 polymerase.	521	6	5.0	1674	21	AAW87912	Human complementar
449	6	5.0	851	22	AAW72617	Carassius auratus	522	6	5.0	1674	21	AAW87912	Human complementar

523	10	22	AAG844008	4.1	5	596	Arabidopsis thalia	596	21	14	AAR45053	Basic (positively
524	10	22	AAG844261	4.1	5	597	Arabidopsis thalia	597	21	14	AAR45054	Basic (positively
525	10	22	AAG844262	4.1	5	598	Arabidopsis thalia	598	21	14	AAR36312	Amphiphilic ion ch
526	10	22	AAG844263	4.1	5	599	Arabidopsis thalia	599	21	14	AAR36313	Amphiphilic ion ch
527	10	22	AAG844264	4.1	5	600	Arabidopsis thalia	600	21	14	AAR31083	C-terminal substd.
528	10	22	AAG84476	4.1	5	601	Arabidopsis thalia	601	21	14	AAR31084	C-terminal substd.
529	11	9	AAP82891	4.1	5	602	N-terminal of hg-C	602	21	14	AAR35301	Amphiphilic peptid
530	11	12	AAR11923	4.1	5	603	B. burgdorferi pc-	603	21	14	AAR35302	Amphiphilic peptid
531	11	12	AAR12103	4.1	5	604	B. burgdorferi pc-	604	21	14	AAR39015	Amphiphilic peptid
532	11	20	AAY31331	4.1	5	605	B. subtilis surfac	605	21	14	AAR39016	Biologically activ
533	11	20	AAW67678	4.1	5	606	LXHL signature mo	606	21	15	AAR55907	Biologically activ
534	11	21	AAW88539	4.1	5	607	NCAM Igl binding p	607	21	15	AAR55908	Ion channel formin
535	11	22	AAW86343	4.1	5	608	G. suboxydans DSM	608	21	15	AAR50483	Amphiphilic pepti
536	12	19	AAW80588	4.1	5	609	Peptide fragment f	609	21	15	AAR50484	Amphiphilic peptid
537	12	22	AAW67000	4.1	5	610	Fl-scd2K peptide.	610	21	15	AAR50367	Amphiphilic peptid
538	13	7	AAP61493	4.1	5	611	Sequence of LDH-C4	611	21	15	AAR50368	Amphiphilic pepti
539	13	17	AAR98232	4.1	5	612	Tau protein phosph	612	21	15	AAR50369	Amphiphilic peptid
540	13	21	AAB21965	4.1	5	613	Phosphorylated tau	613	21	15	AAR50370	Amphiphilic pepti
541	14	10	AAP97794	4.1	5	614	Sequence of fragme	614	21	15	AAR55623	Amphiphilic peptid
542	14	14	AAR32977	4.1	5	615	Mastoparan analogu	615	21	15	AAR58986	Peptide which neut
543	14	14	AAR32983	4.1	5	616	Mastoparan analogu	616	21	16	AAR90076	Peptide which neut
544	14	16	AAR70461	4.1	5	617	VH sequence of ant	617	21	16	AAR83846	Cancer treating, a
545	15	12	AAW14809	4.1	5	618	ves oncogene prote	618	21	16	AAR83847	(KLKALG)3 peptide
546	15	12	AAR13979	4.1	5	619	[Leu12,Lys14]Melit	619	21	16	AAR83848	Ion channel formin
547	15	16	AAR61470	4.1	5	620	[Leu12, Lys14] m	620	21	20	AAV10672	Peptide used to ma
548	15	19	AAY20842	4.1	5	621	Human neurofilamen	621	21	20	AAV10671	Peptide used to ma
549	15	21	AAB07617	4.1	5	622	A human alpha-heli	622	22	20	AAV19067	Lecithin:cholester
550	15	21	AAV93013	4.1	5	623	Transforming growt	623	22	20	AAV18972	Lecithin:cholester
551	15	21	AAB03303	4.1	5	624	Human epitope Rb50	624	22	20	AAV18972	Lecithin:cholester
552	15	21	AAV52604	4.1	5	625	v-fes encoded onco	625	22	20	AAV18736	Lecithin:cholester
553	15	21	AAV52671	4.1	5	626	v-fes encoded onco	626	22	20	AAV18736	Lecithin:cholester
554	15	22	AAU00751	4.1	5	627	Human HTAU40 (R2-R	627	22	20	AAV18550	Lecithin:cholester
555	15	22	AAU00752	4.1	5	628	Human HTAU40 (R2-R	628	22	20	AAV18473	Lecithin:cholester
556	15	22	AAU00753	4.1	5	629	Human HTAU40 (R2-R	629	22	20	AAV18455	Lecithin:cholester
557	16	19	AAW04534	4.1	5	630	HPC heavy chain N-	630	22	20	AAV19226	Lecithin:cholester
558	16	19	AAW04533	4.1	5	631	Human microtubule	631	22	20	AAV19244	Lecithin:cholester
559	17	17	AAW04532	4.1	5	632	HPC transgenic mou	632	22	20	AAV19321	Lecithin:cholester
560	17	17	AAR98230	4.1	5	633	Tau protein phosph	633	22	21	AAV69292	Peptide encoded by
561	17	20	AAV58642	4.1	5	634	Secreted protein e	634	22	22	AAU00778	Human TAU derived
562	17	20	AAV25450	4.1	5	635	Human secreted pro	635	23	20	AAW87840	Bcl-2 related prot
563	17	20	AAV35881	4.1	5	636	Signal peptide of	636	23	21	AAW51961	Human secreted pro
564	17	20	AAV12669	4.1	5	637	Human 5' EST secre	637	23	22	AAW91392	Tachykinins peptid
565	17	20	AAV11368	4.1	5	638	Human 5' EST secre	638	23	22	AAW74157	LMW5-HL BH2 domain
566	17	20	AAV11710	4.1	5	639	Peptide encoded by	639	24	22	AAW83434	Part of elastomeri
567	17	20	AAV12515	4.1	5	640	Human 5' EST signa	640	24	20	AAW73539	PR-R major fragmen
568	17	20	AAV04165	4.1	5	641	Human secreted pro	641	24	20	AAW83434	PR-R major amino a
569	17	20	AAV04147	4.1	5	642	Human secreted pro	642	24	22	AAW35797	Peptide #9834 enco
570	17	21	AAW00013	4.1	5	643	Human secreted pro	643	24	22	AAU04337	ATP-binding cassat
571	17	21	AAW64645	4.1	5	644	Human 48-19-3-G1-F	644	25	16	AAW72322	Tachykinins peptid
572	18	22	AAU04088	4.1	5	645	Signal peptide enc	645	25	16	AAW86865	Laccase internal p
573	18	14	AAR54456	4.1	5	646	Disclosed Amb a 1.	646	25	21	AAW13525	Secreted protein e
574	18	14	AAR54456	4.1	5	647	Systemin. lycoper	647	25	21	AAV99868	Farnesoid X recept
575	18	15	AAR47084	4.1	5	648	Eukaryotic folding	648	25	21	AAV99868	Human nuclear rece
576	18	15	AAW35734	4.1	5	649	Sequence of the ju	649	25	22	AAW29268	Peptide #3217 enco
577	18	19	AAW62033	4.1	5	650	pD3 specific pept	650	25	22	AAW04500	Peptide #3305 enco
578	18	20	AAW99102	4.1	5	651	Tomato systemin.	651	26	17	AAW99001	Peptide #3182 enco
579	18	20	AAW97629	4.1	5	652	Tomato peptide hor	652	26	18	AAW31703	Herpes simplex vir
580	18	20	AAW97630	4.1	5	653	Systemin-like pept	653	26	20	AAW27809	Human secreted pro
581	18	21	AAW97631	4.1	5	654	Systemin-like pept	654	26	20	AAW73540	PR-R minor fragmen
582	18	21	AAW30686	4.1	5	655	Amino acid sequenc	655	26	20	AAW83435	PR-R minor amino a
583	18	21	AAW30687	4.1	5	656	Amino acid sequenc	656	26	22	AAU00770	HCG antigenic pept
584	18	21	AAW30688	4.1	5	657	Amino acid sequenc	657	26	22	AAW69448	Human TAU derived
585	18	22	AAW92381	4.1	5	658	Miscellaneous pept	658	27	19	AAW93470	HCG antigenic pept
586	18	22	AAW92381	4.1	5	659	Cancer treating, a	659	27	22	AAW20329	Synthetic antigeni
587	20	16	AAW13196	4.1	5	660	Fragment of p53 bi	660	27	22	AAW34621	Peptide #6763 enco
588	20	19	AAW69447	4.1	5	661	HCG antigenic pept	661	27	22	AAU01180	Peptide #8658 enco
589	20	19	AAW57347	4.1	5	662	Human Wbpl immunog	662	27	22	AAU01182	Synthetic HCG anti
590	20	21	AAW93468	4.1	5	663	Synthetic antigeni	663	28	20	AAV19725	Human chorionic go
591	20	21	AAW90974	4.1	5	664	Human periplasmic	664	29	19	AAW50235	SEQ ID NO 443 from
592	20	21	AAV51391	4.1	5	665	Human S182 5'-UTR	665	29	20	AAV45334	Peptide for Tn ant
593	20	21	AAV50993	4.1	5	666	Potato pr17-WT pro	666	29	20	AAV27770	Human secreted pro
594	20	22	AAU02874	4.1	5	667	Human Chorionic Go	667	29	20	AAV27770	Human secreted pro
595	20	22	AAU01177	4.1	5	668	Synthetic human ch	668	29	20	AAW83089	Peptide from the 3

669	4.1	29	20	AAW83091	Peptide from the 3	742	5	4.1	43	21	AAW94692	Human zslg93 epit
670	4.1	30	5	AAW40384	Sequence of synthe	743	5	4.1	43	22	AAW15008	Peptide #1442 enco
671	4.1	30	12	AAW14803	fes oncogene prote	744	5	4.1	43	22	AAW17615	Peptide #1409 enco
672	4.1	30	20	AAW36687	Fragment of human	745	5	4.1	43	22	AAW27445	Peptide #1482 enco
673	4.1	30	20	AAW25325	Human pancreatic p	746	5	4.1	43	22	AAW30133	Peptide #1470 enco
674	4.1	30	20	AAW12930	Amino acid sequenc	747	5	4.1	43	22	AAW02736	Peptide #1418 enco
675	4.1	30	20	AAW83090	Peptide from the 3	748	5	4.1	43	22	AAW05274	Peptide #3956 enco
676	4.1	30	21	AAW52601	v-fes encoded onco	749	5	4.1	43	22	AAW77787	Human colon cancer
677	4.1	30	21	AAW00775	Human TAU derived	750	5	4.1	44	22	AAW34270	Peptide #8307 enco
678	4.1	31	22	AAW55106	Tau protein fragme	751	5	4.1	45	18	AAW20450	H. pylori secreted
679	4.1	31	22	AAW12834	HIV protecting vac	752	5	4.1	45	20	AAW27663	Human secreted pro
680	4.1	32	12	AAW12834	SIV-derived lipope	753	5	4.1	45	20	AAW12762	Human 5' EST secre
681	4.1	32	20	AAW26637	Human secreted pro	754	5	4.1	45	21	AAW57037	Arabidopsis thalia
682	4.1	32	21	AAW33995	Human secreted pro	755	5	4.1	46	21	AAW37356	Human secreted pro
683	4.1	32	22	AAW44627	Human secreted pro	756	5	4.1	46	22	AAW31704	Peptide #5741 enco
684	4.1	32	22	AAW61947	Modified [Ala17]HG	757	5	4.1	46	22	AAW31704	Human colon cancer
685	4.1	33	21	AAW09315	Hepatitis GB virus	758	5	4.1	46	22	AAW67632	Human secreted pro
686	4.1	33	21	AAW58301	Human p160 coactiv	759	5	4.1	47	20	AAW13000	Human secreted pro
687	4.1	33	21	AAW64883	Human 5' EST relat	760	5	4.1	47	21	AAW07623	A human alpha-hell
688	4.1	34	21	AAW32440	Human secreted pro	761	5	4.1	48	20	AAW07623	Amino acid sequenc
689	4.1	35	10	AAW94257	Amino acid sequenc	762	5	4.1	48	21	AAW02923	Fragment of human
690	4.1	35	10	AAW94257	S protein from lam	763	5	4.1	48	21	AAW27581	Human secreted pro
691	4.1	35	19	AAW75127	Human secreted pro	764	5	4.1	48	21	AAW18419	Peptide #4853 enco
692	4.1	35	20	AAW08477	Human BS274 protei	765	5	4.1	48	22	AAW21905	Peptide #8339 enco
693	4.1	35	21	AAW45087	Human secreted pro	766	5	4.1	48	22	AAW30896	Peptide #4933 enco
694	4.1	35	21	AAW45088	Human secreted pro	767	5	4.1	48	22	AAW38233	Peptide #12270 enco
695	4.1	35	22	AAW33148	Eucalyptus grandis	768	5	4.1	48	22	AAW06018	Peptide #4700 enco
696	4.1	36	10	AAW91353	Peptide #9359 enco	769	5	4.1	49	8	AAW70036	Secretory signal s
697	4.1	36	22	AAW16855	Amino acid sequenc	770	5	4.1	49	22	AAW23855	Human EST encoded
698	4.1	36	22	AAW29139	Peptide #3089 enco	771	5	4.1	49	22	AAW31651	C glutamicum prote
699	4.1	36	22	AAW04371	Peptide #3176 enco	772	5	4.1	49	22	AAW56577	Amino acid sequenc
700	4.1	36	22	AAW77662	Peptide #3053 enco	773	5	4.1	50	21	AAW06603	Arabidopsis thalia
701	4.1	37	13	AAW29218	Human colon cancer	774	5	4.1	50	21	AAW55275	Human foetal prote
702	4.1	37	13	AAW29218	Thr(13)His(21)Leu(775	5	4.1	51	21	AAW55275	Arabidopsis thalia
703	4.1	37	13	AAW29218	Thr(13)Arg(18)His(776	5	4.1	51	21	AAW60308	Arabidopsis thalia
704	4.1	37	14	AAW38822	Thr13, His21, Leu2	777	5	4.1	51	21	AAW61663	Arabidopsis thalia
705	4.1	37	14	AAW38824	Thr13, Arg18, His2	778	5	4.1	51	21	AAW30271	Human secreted pro
706	4.1	37	19	AAW74604	Amino acid sequenc	779	5	4.1	51	22	AAW37342	Chaperone cpn60 pr
707	4.1	37	19	AAW74604	Amino acid sequenc	780	5	4.1	52	21	AAW44032	Human cancer assoc
708	4.1	37	20	AAW22455	Human secreted pro	781	5	4.1	52	21	AAW66029	Telomerase associa
709	4.1	37	20	AAW22457	Human secreted pro	782	5	4.1	52	22	AAW18899	Peptide #5333 enco
710	4.1	37	20	AAW90160	Amino acid sequenc	783	5	4.1	52	22	AAW31438	Peptide #5475 enco
711	4.1	37	20	AAW90162	Human amylin agoni	784	5	4.1	53	21	AAW56576	Arabidopsis thalia
712	4.1	37	20	AAW88882	Polypeptide fragme	785	5	4.1	53	21	AAW06421	Human foetal prote
713	4.1	37	21	AAW44787	Human secreted pro	786	5	4.1	54	17	AAW01176	Serine protease pf
714	4.1	37	21	AAW45344	Human secreted pro	787	5	4.1	54	20	AAW27827	Human secreted pro
715	4.1	37	21	AAW18595	Amino acid sequenc	788	5	4.1	54	21	AAW57910	Arabidopsis thalia
716	4.1	37	21	AAW18597	Amino acid sequenc	789	5	4.1	54	21	AAW61712	Arabidopsis thalia
717	4.1	38	15	AAW4065	Non-A, non-B hepat	790	5	4.1	54	22	AAW14086	Peptide #520 enco
718	4.1	38	21	AAW36559	Arabidopsis thalia	791	5	4.1	54	22	AAW17999	Peptide #4433 enco
719	4.1	38	22	AAW20610	Peptide #7044 enco	792	5	4.1	54	22	AAW26493	Peptide #530 enco
720	4.1	38	22	AAW31361	Peptide #5398 enco	793	5	4.1	54	22	AAW30510	Peptide #4547 enco
721	4.1	38	22	AAW35598	Peptide #9635 enco	794	5	4.1	54	22	AAW36572	Peptide #10609 enco
722	4.1	38	22	AAW36701	Peptide #10738 enc	795	5	4.1	54	22	AAW01826	Peptide #508 enco
723	4.1	38	22	AAW76624	Human colon cancer	796	5	4.1	54	22	AAW05640	Human colon cancer
724	4.1	38	22	AAW31646	Amino acid sequenc	797	5	4.1	54	22	AAW76999	Flea serine protea
725	4.1	39	21	AAW13631	Arabidopsis thalia	798	5	4.1	54	22	AAW50572	Human secreted pro
726	4.1	39	21	AAW01053	Human secreted pro	799	5	4.1	55	20	AAW36294	Human colon cancer
727	4.1	40	20	AAW25654	Carpinus betulus a	800	5	4.1	55	21	AAW53511	Haem protein relat
728	4.1	40	21	AAW09414	Hepatitis GB virus	801	5	4.1	55	22	AAW04659	Protein encoded by
729	4.1	40	22	AAW21694	Peptide #8128 enco	802	5	4.1	56	21	AAW70398	Peptide #424 enco
730	4.1	40	22	AAW38005	Peptide #12042 enc	803	5	4.1	56	22	AAW13990	Peptide #854 enco
731	4.1	41	20	AAW49769	Compact structure	804	5	4.1	56	22	AAW14420	Human EST encoded
732	4.1	41	21	AAW88087	Yeast 70 kd outer	805	5	4.1	56	22	AAW24354	Peptide #433 enco
733	4.1	41	21	AAW43830	M. pneumoniae ygd	806	5	4.1	56	22	AAW26396	Peptide #870 enco
734	4.1	41	21	AAW52276	Peptide #5337 enco	807	5	4.1	56	22	AAW26833	Peptide #413 enco
735	4.1	41	22	AAW18903	Peptide #5480 enco	808	5	4.1	56	22	AAW01731	Peptide #829 enco
736	4.1	41	22	AAW31443	Peptide #8320 enco	809	5	4.1	56	22	AAW02147	Human cytomegalovi
737	4.1	41	22	AAW34283	Transdominant effe	810	5	4.1	57	17	AAW88669	Human zslg93 epit
738	4.1	41	22	AAW45946	Yeast 70kd outer m	811	5	4.1	57	22	AAW15950	Peptide #2384 enco
739	4.1	41	22	AAW35078	zea mays protein f	812	5	4.1	57	22	AAW28453	Peptide #2490 enco
740	4.1	42	21	AAW27049	Human colon cancer	813	5	4.1	57	22	AAW37175	Peptide #11212 enc
741	4.1	43	20	AAW02746	Human secreted pro	814	5	4.1	57	22	AAW03688	Peptide #2370 enco

815	5	4.1	58	21	AAB40482	Human OREF ORF246	888	5	4.1	73	21	AAG00524	Human secreted pro
816	5	4.1	58	21	AAB43317	Human OREF ORF3081	889	5	4.1	73	22	AAM41980	Human polypeptide
817	5	4.1	58	21	AAG11425	Arabidopsis thalia	890	5	4.1	73	22	AAG74694	Human colon cancer
818	5	4.1	58	21	AAG50021	Arabidopsis thalia	891	5	4.1	74	20	AAV57463	Antimicrobial pept
819	5	4.1	58	22	AAM17066	Peptide #3500 enco	892	5	4.1	74	20	AAV57464	Antimicrobial pept
820	5	4.1	58	22	AAM17130	Peptide #3564 enco	893	5	4.1	74	20	AAV60440	Human normal bladd
821	5	4.1	58	22	AAM29560	Peptide #3597 enco	894	5	4.1	74	20	AAV11580	Human novel protei
822	5	4.1	58	22	AAM29623	Peptide #3660 enco	895	5	4.1	74	22	AAU14313	Human novel protei
823	5	4.1	58	22	AAM04768	Peptide #3507 enco	896	5	4.1	74	22	AAU14549	Amino acid sequenc
824	5	4.1	58	22	AAM04825	Human colon cancer	897	5	4.1	75	18	AAW27980	Human secreted pro
825	5	4.1	58	22	AAG74158	Human colon cancer	898	5	4.1	75	20	AAV13046	IKK-alpha polypept
826	5	4.1	58	22	AAG74805	Human secreted pro	899	5	4.1	75	20	AAW96169	Human prostate can
827	5	4.1	59	20	AAV07888	Zeas may protein f	900	5	4.1	75	21	AAV56727	Human secreted pro
828	5	4.1	59	20	AAV25990	Peptide #9489 enco	901	5	4.1	75	21	AAV33729	Arabidopsis thalia
829	5	4.1	59	22	AAM35452	Human cytomagalovi	902	5	4.1	75	21	AAV22791	Arabidopsis thalia
830	5	4.1	59	22	AAB11464	CENP-B peptide. S	903	5	4.1	75	21	AAV22791	Arabidopsis thalia
831	5	4.1	60	14	AAV32973	Peptide #2019 enco	904	5	4.1	75	21	AAV22791	Arabidopsis thalia
832	5	4.1	60	22	AAM15585	Peptide #2014 enco	905	5	4.1	75	22	AAM15595	Peptide #2029 enco
833	5	4.1	60	22	AAM28077	Peptide #2011 enco	906	5	4.1	75	22	AAM28092	Peptide #2129 enco
834	5	4.1	60	22	AAM03329	Arabidopsis thalia	907	5	4.1	75	22	AAM03340	C glutamicum prote
835	5	4.1	61	21	AAG48248	Human secreted pro	908	5	4.1	75	22	AAV00092	Human secreted pro
836	5	4.1	61	21	AAG02241	Human colon cancer	909	5	4.1	76	20	AAV02755	Human zsig83 epit
837	5	4.1	61	22	AAG76480	Human secreted pro	910	5	4.1	76	21	AAV94694	A human alpha-heli
838	5	4.1	62	21	AAG03666	Arabidopsis thalia	911	5	4.1	76	21	AAV07613	Arabidopsis thalia
839	5	4.1	63	21	AAG20211	Arabidopsis thalia	912	5	4.1	76	21	AAV41329	Arabidopsis thalia
840	5	4.1	63	21	AAG30061	Synechocystis tyro	913	5	4.1	76	21	AAV57267	Arabidopsis thalia
841	5	4.1	63	21	AAV77896	Chicken metallothi	914	5	4.1	76	21	AAV03592	Human secreted pro
842	5	4.1	63	21	AAV57811	Human kidney relat	915	5	4.1	76	22	AAV74264	Human colon cancer
843	5	4.1	63	22	AAM42583	Human gene 12-enco	916	5	4.1	76	22	AAV76434	Staphylococcus aur
844	5	4.1	63	22	AAG73406	Epitope of human C	917	5	4.1	77	18	AAW28041	Human endometrium
845	5	4.1	64	14	AAV30639	Girdwood S.A.virus	918	5	4.1	77	20	AAV60199	Human colon cancer
846	5	4.1	64	19	AAV70476	Sindbis virus E3 p	919	5	4.1	77	22	AAV74942	Human PAPB#4 prote
847	5	4.1	64	19	AAV70483	South African Arbo	920	5	4.1	78	20	AAV22523	Human 5' EST secre
848	5	4.1	64	19	AAV70469	Peptide #6944 enco	921	5	4.1	78	20	AAV12633	Human colon cancer
849	5	4.1	64	22	AAM20510	Peptide #8561 enco	922	5	4.1	78	22	AAV75666	Human secreted pro
850	5	4.1	64	22	AAM34524	Peptide #9290 enco	923	5	4.1	79	20	AAV12993	Breast and ovarian
851	5	4.1	64	22	AAV35253	Human zsig83 epit	924	5	4.1	79	21	AAV58924	Human secreted pro
852	5	4.1	65	21	AAV94689	Arabidopsis thalia	925	5	4.1	79	21	AAV34138	Human zsig83 epit
853	5	4.1	65	21	AAV25858	Human secreted pro	926	5	4.1	79	21	AAV94690	Human protein sequ
854	5	4.1	65	21	AAG00533	Peptide #7993 enco	927	5	4.1	79	22	AAM25542	Acanthamoeba caste
855	5	4.1	65	22	AAM21559	Peptide #11870 enc	928	5	4.1	79	22	AAV70689	S. pneumoniae puri
856	5	4.1	65	22	AAV37833	Human 5' EST secre	929	5	4.1	80	19	AAV38733	Human endometrium
857	5	4.1	66	20	AAV12117	Arabidopsis thalia	930	5	4.1	80	20	AAV60276	Zeas may protein f
858	5	4.1	66	21	AAV61695	Human secreted pro	931	5	4.1	80	21	AAV26771	IKK-alpha polypept
859	5	4.1	66	21	AAV00769	Peptide #8738 enco	932	5	4.1	81	20	AAW96168	Polypeptide fragme
860	5	4.1	66	22	AAV34701	Human secreted pro	933	5	4.1	81	20	AAW88832	Polypeptide fragme
861	5	4.1	67	21	AAV03366	Human normal bladd	934	5	4.1	81	21	AAV32782	Eucalyptus grandis
862	5	4.1	68	20	AAV60351	Arabidopsis thalia	935	5	4.1	81	21	AAV07621	A human alpha-heli
863	5	4.1	68	21	AAV38479	Peptide #44 enco	936	5	4.1	81	21	AAV26584	Arabidopsis thalia
864	5	4.1	68	22	AAV13610	Peptide #44 enco	937	5	4.1	82	19	AAV74944	Human secreted pro
865	5	4.1	68	22	AAV26007	Peptide #42 enco	938	5	4.1	82	21	AAV37946	Chlamydia trachoma
866	5	4.1	68	22	AAV01360	Human foetal prote	939	5	4.1	82	21	AAV00770	Human secreted pro
867	5	4.1	68	22	AAV06379	Human gene 8 enco	940	5	4.1	82	21	AAV00772	Human secreted pro
868	5	4.1	68	22	AAE03059	Human gene 8 enco	941	5	4.1	82	21	AAV03269	Human secreted pro
869	5	4.1	68	22	AAE03090	Human secreted pro	942	5	4.1	82	21	AAV14726	Peptide #1160 enco
870	5	4.1	69	19	AAV75015	Zeas may protein f	943	5	4.1	82	22	AAV27149	Peptide #1186 enco
871	5	4.1	69	21	AAV27048	S. pneumoniae prot	944	5	4.1	83	18	AAW20988	H. pylori cytoplas
872	5	4.1	69	21	AAV01887	Human colon cancer	945	5	4.1	83	19	AAV74785	Human secreted pro
873	5	4.1	70	18	AAV11327	Human colon cancer	946	5	4.1	83	20	AAV12632	Human 5' EST secre
874	5	4.1	70	21	AAV53869	Arabidopsis thalia	947	5	4.1	83	21	AAV58037	DDC3 (dopa decarbo
875	5	4.1	70	21	AAV57909	Human novel protei	948	5	4.1	83	22	AAV92972	Human protein sequ
876	5	4.1	70	22	AAU14295	Human novel protei	949	5	4.1	83	22	AAV50241	Human breast cance
877	5	4.1	70	22	AAU14531	Human novel protei	950	5	4.1	84	17	AAW01208	Serine protease pf
878	5	4.1	70	22	AAV76521	Human colon cancer	951	5	4.1	84	18	AAW00945	CMV500-4heptadCREB
879	5	4.1	70	22	AAV77157	Human colon cancer	952	5	4.1	84	21	AAV16300	Eucalyptus grandis
880	5	4.1	70	22	AAE01718	Human gene 9 enco	953	5	4.1	84	21	AAV58639	Arabidopsis thalia
881	5	4.1	71	21	AAV07611	A human alpha-heli	954	5	4.1	84	21	AAV57209	Arabidopsis thalia
882	5	4.1	72	19	AAV85793	S. pneumoniae deri	955	5	4.1	84	21	AAV02176	Human secreted pro
883	5	4.1	72	21	AAV18896	Zeas may protein f	956	5	4.1	84	21	AAV02380	Human secreted pro
884	5	4.1	72	21	AAV25311	Zeas may protein f	957	5	4.1	84	21	AAV76534	Human colon cancer
885	5	4.1	72	21	AAV56876	Zeas may protein f	958	5	4.1	84	22	AAV59605	Flea serine protea
886	5	4.1	72	21	AAV76352	Fragment Of human	959	5	4.1	85	19	AAV59652	Amino acid sequenc
887	5	4.1	73	21	AAV40163	Human secreted pro	960	5	4.1	85	20	AAV59643	Secreted protein e

DE Human secreted protein encoded by gene 17 clone HPMQ91.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

XX WO9840483-A2.

XX 17-SEP-1998.

XX 12-MAR-1998; 98WO-US04858.

XX 19-DEC-1997; 97US-0068368.

XX 14-MAR-1997; 97US-0040710.

XX 30-MAY-1997; 97US-0040762.

XX 30-MAY-1997; 97US-0048100.

XX 30-MAY-1997; 97US-0048189.

XX 30-MAY-1997; 97US-0048357.

XX 30-MAY-1997; 97US-0050934.

XX 06-JUN-1997; 97US-0048970.

XX 05-SEP-1997; 97US-0057765.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;

XX Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;

XX Wei YF, Young PE, Zeng Z;

XX WPI: 1998-520811/44.

XX N-PSDB; AAV34302.

XX Isolated human poly(nucleotide(s)) encoding secretory peptide(s) -
 PT used to develop products for the diagnosis and treatment of e.g.
 PT inflammation, cancers, CNS disorders or immune system disorders

XX Claim 1; Page 162-163; 20lpp; English.
 XX This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. AAV34277) for increasing the stability of the fused
 CC protein as compared to the human protein only.
 CC The invention relates to 28 novel genes and their fragments (nucleic
 CC acid sequences: AAV34286-V34325; amino acid sequences AAV75196-W75235)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 28
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV34286 for described uses).

XX Sequence 121 AA;

Query Match 54.5%; Score 66; DB 19; Length 121;

Best Local Similarity 100.0%; Pred. No. 1.1e-57;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIMLFTAILAFSLAQSGFAGVCKEPEEVVPGGGRKRDPLYLQLQRLFKSHSLEGL 60

Db 1 mrmlftailafslaqsfagvckepqevvpgggrskrdpdyqlqlrflkshsslegl 60

Qy 61 LKALSQ 66

Db 61 lkalsq 66

RESULT 3

AAW97213

ID AAW97213 standard; Protein; 121 AA.

XX AAW97213;

XX 07-MAY-1999 (first entry)

XX A human zneurokl polypeptide.

XX Human; zneurokl; neurokinin B; prohormone convertase; cell growth;
 KW modulation; inflammation; noinception; emesis; contraction;
 KW hormone secretion; DNA synthesis; inositol phosphate turnover;
 KW arachidonate release; phospholipase-C activation; gastric emptying;
 KW human neutrophil activation; ADCC capability;
 KW superoxide anion production; gene therapy.

XX Homo sapiens.

XX WO9855612-A1.

XX 10-DEC-1998.

XX 28-MAY-1998; 98WO-US10842.

XX 02-JUN-1997; 97US-0048290.

XX (ZYMO) ZYMOGENETICS INC.

XX Sheppard PO;

XX WPI: 1999-070268/06.

XX N-PSDB; AAX15447.

XX New isolated neurokinin polypeptides, zneurokl - used to develop
 PT products for modulating e.g. inflammation, noinception, emesis,
 PT muscle contraction, hormone secretion, DNA synthesis or cell growth

XX Claim 3; Page 76-77; 100pp; English.

XX The present sequence represents a human zneurokl polypeptide. The
 CC polypeptide releases a neurokinin B polypeptide in the presence
 CC of a prohormone convertase capable of cleaving dibasic amino
 CC acids. The zneurokl polypeptides can be used for modulating inflammation,
 CC noinception or emesis. The polypeptides, fragments, fusion proteins,
 CC agonists, antagonists or antibodies may also modulate contraction,
 CC hormone secretion, DNA synthesis or cell growth, inositol phosphate
 CC turnover, arachidonate release, phospholipase-C activation, gastric
 CC emptying, human neutrophil activation or ADCC capability, or superoxide
 CC anion production. The polynucleotides can also be used for gene therapy.
 CC The products can also be used for detection, diagnosis and screening
 CC assays.

XX Sequence 121 AA;

Query Match 54.5%; Score 66; DB 20; Length 121;

Best Local Similarity 100.0%; Pred. No. 1.1e-57;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIMLFTAILAFSLAQSGFAGVCKEPEEVVPGGGRKRDPLYLQLQRLFKSHSLEGL 60

Db 1 mrmlftailafslaqsfagvckepqevvpgggrskrdpdyqlqlrflkshsslegl 60

Qy 61 LKALSQ 66

Db 61 lkalsq 66

RESULT 4

AAW74413


```

Db      61 lkalsq 66

RESULT 6
AAW96144
ID      AAW96144 standard; Protein; 122 AA.
XX      AC
XX      AAW96144;
XX      AC
DT      27-APR-1999 (first entry)
XX      DE
XX      Human preprotachykinin B.
XX      KW
XX      Preprotachykinin B; PPT-B; neoplastic disorder;
XX      neurological disorder; Alzheimer's disease; amnesia;
XX      cerebral neoplasms; dementia; depression; Down's syndrome;
XX      Huntington's disease; multiple sclerosis; Parkinson's disease;
XX      paranoid psychoses; schizophrenia; Tourette's disorder; angina;
XX      anaphylactic shock; asthma; cardiovascular shock;
XX      myocardial infarction; migraine.
XX      OS
XX      Homo sapiens.
XX      FH
XX      Key
XX      Location/Qualifiers
XX      Misc-difference 104
XX      /label= Leu, Ser or Trp
XX      PN
XX      WO9857986-A2.
XX      PD
XX      23-DEC-1998.
XX      XX
XX      19-JUN-1998; 98WO-US12855.
XX      XX
XX      19-JUN-1997; 97US-0879995.
XX      PR
XX      (INCY-) INCYTE PHARM INC.
XX      PA
XX      Hillman JJ, Kaser MR, Lal P;
XX      PI
XX      WPI: 1999-080948/07.
XX      DR
XX      N-PSDB; AAX08906.
XX      XX
XX      New human preprotachykinin B - useful for treating neurological
XX      disorders and cancer
XX      PS
XX      Claim 1; Page 48-49; 57pp; English.
XX      CC
XX      Human preprotachykinin B (PPT-B) can be used to treat a
XX      neurological disorder. Antagonists of PPT-B can also be used in
XX      the treatment of neoplastic disorders. Particular neurological,
XX      disorders include akathisia, Alzheimer's disease, amnesia,
XX      amyotrophic lateral sclerosis, bipolar disorder, cataplexia,
XX      cerebral neoplasms, dementia, depression, Down's syndrome, tardive
XX      dyskinesia, dystonias, Huntington's disease, multiple sclerosis,
XX      neurofibromatosis, Parkinson's disease, paranoid psychoses,
XX      schizophrenia, and Tourette's disorder. PPT-B or its agonist can
XX      also be used to treat angina, anaphylactic shock, arrhythmias,
XX      asthma, cardiovascular shock, Cushing's syndrome, hypertension,
XX      hypoglycemia, myocardial infarction, migraine and pheochromocytoma.
XX      SQ
XX      Sequence 122 AA;

Query Match      54.5%; Score 66; DB 20; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRIMLFTAILAFSLAQSGAVCKPEQEVPGGRSKRDPDLYQLLQRLFKSHSLEGL 60
        |||||||
Db      1 mrimlftailafslaqsgavckpeqevpggrskrdpdlyqlrlfkshslegl 60
        |||||||

QY      61 LKALSQ 66
        |||||

```

Db 61 lkalsq 66

RESULT 7

AAB33445

ID AAB33445 standard; Protein; 135 AA.

XX AC

XX AAB33445;

XX AC

DT 29-JAN-2001 (first entry)

XX DE

XX Human PRO1155 protein UNQ585 SEQ ID NO:157.

XX XX

Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 dermatological; antiarthritic; antirheumatic; immunosuppressive;
 haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
 antianemic; hepatotropic; viricide; antipsoriatic; antiallergic;
 antianastemic; systemic lupus erythematosus; rheumatoid arthritis;
 osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
 idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 autoimmune thrombocytopenia; immune-mediated renal disease;
 demyelinating disease; hepatobiliary disease; whipple's disease;
 inflammatory bowel disease; gluten-sensitive enteropathy;
 autoimmune disease; immune-mediated skin disease; allergic disease;
 immunological disease; transplantation associated disease;
 graft rejection; graft-versus-host-disease.

XX OS

XX Homo sapiens.

XX XX

XX WO200053758-A2.

XX PD

XX 14-SEP-2000.

XX XX

XX 02-MAR-2000; 2000WO-US05841.

XX XX

XX 08-MAR-1999; 99WO-US05028.

XX PR

XX 10-MAR-1999; 99US-0123618.

XX PR

XX 12-MAR-1999; 99US-0123957.

XX PR

XX 23-MAR-1999; 99US-0125775.

XX PR

XX 12-APR-1999; 99US-0128849.

XX PR

XX 20-APR-1999; 99WO-US08615.

XX PR

XX 28-APR-1999; 99US-0131445.

XX PR

XX 04-MAY-1999; 99US-0132371.

XX PR

XX 14-MAY-1999; 99US-0134287.

XX PR

XX 02-JUN-1999; 99WO-US12252.

XX PR

XX 23-JUN-1999; 99US-0141037.

XX PR

XX 20-JUL-1999; 99US-0144758.

XX PR

XX 26-JUL-1999; 99US-0145698.

XX PR

XX 28-JUL-1999; 99US-0146222.

XX PR

XX 01-SEP-1999; 99WO-US20111.

XX PR

XX 08-SEP-1999; 99WO-US20594.

XX PR

XX 13-SEP-1999; 99WO-US20944.

XX PR

XX 15-SEP-1999; 99WO-US21090.

XX PR

XX 15-SEP-1999; 99WO-US21547.

XX PR

XX 05-OCT-1999; 99WO-US23089.

XX PR

XX 29-OCT-1999; 99US-0162506.

XX PR

XX 30-NOV-1999; 99WO-US28214.

XX PR

XX 30-NOV-1999; 99WO-US28313.

XX PR

XX 01-DEC-1999; 99WO-US28301.

XX PR

XX 01-DEC-1999; 99WO-US28634.

XX PR

XX 02-DEC-1999; 99WO-US28551.

XX PR

XX 02-DEC-1999; 99WO-US28564.

XX PR

XX 02-DEC-1999; 99WO-US28565.

XX PR

XX 16-DEC-1999; 99WO-US30095.

XX PR

XX 20-DEC-1999; 99WO-US30099.

XX PR

XX 30-DEC-1999; 99WO-US31274.

XX PR

XX 05-JAN-2000; 2000WO-US00219.

XX PR

XX 06-JAN-2000; 2000WO-US00277.

XX PR

XX 11-FEB-2000; 2000WO-US00376.

XX PR

XX 11-FEB-2000; 2000WO-US03565.

XX PR

XX 18-FEB-2000; 2000WO-US04341.

XX PR

[illegible]

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PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091360.
PR 02-JUL-1998; 98US-0091444.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094551.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
XX
PA (GETH ) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX WPI; 2000-072883/06.
DR N-PSDB; AAZ65085.
DR

XX Membrane-bound proteins and related nucleotide sequences -
PT
XX claim 12; Fig 254; 822pp; English.
PS
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
XX Sequence 135 AA;
XX
Query Match 54.5%; Score 66; DB 21; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.2e-57;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRIMLLFTALAFSLAQSGAVCKEPQEEVVPVGGSRKDPDLYQLLQRLFKSHSLEGL 60
Db 1 mrimllftalafslaqsgavckepqeevvpvggskrdpdyqlqlrflkshsleagl 60
QY 61 LKALSQ 66
Db 61 lkalsq 66
XX
RESULT 9
AAB65262
ID AAB65262 standard; Protein; 135 AA.
XX
AC AAB65262;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1155 (UNQ585) protein sequence SEQ ID NO:359.
KW Human; secreted and transmembrane protein; PRO: cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
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PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurley AL, Kijavini IJ, Napier MA, Pan J, Paoni NE;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX WPI; 2001-032160/04.
 DR N-PSDB; AAF44231.
 XX PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 254; 935pp; English.
 XX The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytosolic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF4470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 135 AA;

Query Match 54.5%; Score 66; DB 22; Length 135;
 Best Local Similarity 100.0%; Pred. No. 1.2e-57;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLFTAILAFSLAQSGAVCKEPEVEVPGGGRKRPDLYQLLQRLFKSHSSLEGL 60
 |||||
 Db 1 mrimlftailafslagsgavckepqevvpgggrskrdpdyqlqlrfkshsslegl 60

QY 61 LKALSQ 66
 |||||

Db 61 lkalsq 66

RESULT 10
 AAY12634
 ID AAY12634 standard; Protein; 51 AA.
 XX
 AC AAY12634;
 XX

22-JUN-1999 (first entry)
 Human 5' EST secreted protein SEQ ID NO: 299 from WO 9906553.

Human; secreted protein; EST; expressed sequence tag; diagnosis;
 forensic; gene therapy; chromosome mapping; signal peptide;
 upstream regulatory sequence; cytokine activity; cell proliferation;
 differentiation; haematopoiesis regulation; tissue growth regulation;
 reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;

KW thrombolytic; antiinflammatory; tumour inhibition; antitumour.
 XX Homo sapiens.
 OS
 XX WO9906553-A2.
 PN
 XX 11-FEB-1999.
 PD
 XX 31-JUL-1998; 98WO-IB01237.
 PF
 XX 01-AUG-1997; 97US-0905051.
 PR
 XX (GEST) GENSET.
 PA
 XX Duciert A, Dumas Milne Edwards J, Lacroix B;
 PI
 XX WPI; 1999-153783/13.
 DR N-PSDB; AAX41492.
 XX New nucleic acids encoding human secreted proteins - obtained from
 CC cDNA libraries derived from umbilical cord, lymph ganglia,
 CC lymphocytes and placental tissue
 PT
 XX Claim 34; Page 389; 411pp; English.
 PS

XX AAX41379 to AAX41526 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins, and encode the proteins given in AAY12521 to
 CC AAY12668, respectively. The proteins given represent the signal peptide
 CC and an N-terminal fragment of a secreted protein. The nucleic acid
 CC sequences can be used for producing secreted human gene products. They
 CC can also be used to develop products for diagnosis and therapy. The
 CC proteins obtained may have cytokine activity, cell
 CC proliferation/differentiation activity, haematopoiesis regulating
 CC activity, tissue growth regulating activity, reproductive hormone
 CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, receptor/ligand activity, antiinflammatory
 CC activity, tumour inhibition activity or other activities. The products
 CC can be used in forensic, gene therapy and chromosome mapping procedures.
 CC The sequences can also be used for obtaining corresponding promoter
 CC sequences. The nucleic acids encoding the signal peptide can be used for
 CC directing extracellular secretion of a polypeptide or the insertion of a
 CC polypeptide into a membrane, or importing a polypeptide into a cell.

SQ Sequence 51 AA;

Query Match 40.5%; Score 49; DB 20; Length 51;
 Best Local Similarity 100.0%; Pred. No. 3.5e-41;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIMLFTAILAFSLAQSGAVCKEPEVEVPGGGRKRPDLYQLLQRL 49
 |||||
 Db 1 mrimlftailafslagsgavckepqevvpgggrskrdpdyqlqlr 49

RESULT 11
 AAW74414
 ID AAW74414 standard; Protein; 39 AA.
 XX
 AC AAW74414;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE HPMB091 protein sequence fragment.

HPMB091; neurokinin B precursor; neuronal disorder; CNS related disorder;
 gastrointestinal disorder; cardiovascular disorder; metabolic disorder;
 smooth muscle disorder; inflammatory disorder; cancer; gene therapy.
 XX Homo sapiens.
 OS
 XX EP892053-A2.
 PN
 XX

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endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
Homo sapiens.
WO9840483-A2.
17-SEP-1998.
12-MAR-1998; 98WO-US04858.
19-DEC-1997; 97US-0068368.
14-MAR-1997; 97US-0040710.
14-MAR-1997; 97US-0040762.
30-MAY-1997; 97US-0048100.
30-MAY-1997; 97US-0048189.
30-MAY-1997; 97US-0048357.
30-MAY-1997; 97US-0050934.
06-JUN-1997; 97US-0048970.
05-SEP-1997; 97US-0057765.
(HUMA-) HUMAN GENOME SCI INC.
Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;
Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;
Wei YF, Young PE, Zeng Z;
WPI: 1998-520811/44.
N-PSDB; AAV34302.
Isolated human poly:nucleotide(s) encoding secretory peptide(s) -
used to develop products for the diagnosis and treatment of e.g.
inflammation, cancers, CNS disorders or immune system disorders
Disclosure; Page 19; 201pp; English.
This sequence represents a fragment of a secreted human protein encoded
by the nucleic acid molecule designated Gene 17 (AAV34302). The gene
can be used to generate fusion proteins by linking to the gene to a
human immunoglobulin Fc portion (e.g. AAV34277) for increasing the
stability of the fused protein as compared to the human protein only.
The invention relates to 28 novel genes and their fragments (nucleic
acid sequences: AAV34286-V34325; amino acid sequences AAW75196-W75235)
which are useful for preventing, treating or ameliorating medical
conditions e.g. by protein or gene therapy. Also, pathological
conditions can be diagnosed by determining the amount of the new
polypeptides in a sample or by determining the presence of mutations in
the new polynucleotides. Specific uses are described for each of the 28
polynucleotides, based on which tissues they are most highly expressed in
(see AAV34286 for described uses).
Sequence 36 AA;
Query Match 19.0%; Score 23; DB 19; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 90 MGKRSVPDSDPTDNQENVPSEG 112
Db ||||||
14 mgkrsvpdsdptdnqenvpsfg 36
RESULT 13
AAW75250
ID AAW75250 standard; Protein; 15 AA.
XX AAW75250;
XX AC XX
XX DT
XX DE Fragment of human secreted protein encoded by gene 17.
XX KW Human; secreted protein; fusion protein; gene therapy; protein therapy;

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diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; fetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens.

W09840483-A2.

17-SEP-1998.

12-MAR-1998; 98WO-US04858.

19-DEC-1997; 97US-0068368.

14-MAR-1997; 97US-0040710.

30-MAY-1997; 97US-0040762.

30-MAY-1997; 97US-0048100.

30-MAY-1997; 97US-0048189.

30-MAY-1997; 97US-0048357.

06-JUN-1997; 97US-0050934.

05-SEP-1997; 97US-0048970.

05-SEP-1997; 97US-0057765.

(HUMA-) HUMAN GENOME SCI INC.

Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;

Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;

Wei YF, Young PE, Zeng Z;

WPI; 1998-520811/44.

N-PSDB; AAV34302.

Isolated human poly:nucleotide(s) encoding secretory peptide(s) -

used to develop products for the diagnosis and treatment of e.g.

inflammation, cancers, CNS disorders or immune system disorders

Disclosure; Page 19; 201pp; English.

This sequence represents a fragment of a secreted human protein encoded

by the nucleic acid molecule designated Gene 17 (AAV34302). The gene

can be used to generate fusion proteins by linking to the gene to a

human immunoglobulin Fc portion (e.g. AAV34277) for increasing the

stability of the fused protein as compared to the human protein only.

The invention relates to 28 novel genes and their fragments (nucleic

acid sequences: AAV34286-V34325; amino acid sequences AAV75196-W75235)

which are useful for preventing, treating or ameliorating medical

conditions e.g. by protein or gene therapy. Also, pathological

conditions can be diagnosed by determining the amount of the new

polypeptides in a sample or by determining the presence of mutations in

the new polynucleotides. Specific uses are described for each of the 28

polynucleotides, based on which tissues they are most highly expressed in

(see AAV34286 for described uses).

Sequence 15 AA;

Query Match 8.3%; Score 10; DB 19; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.0053;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

DT

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DE

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KW

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KW

KW

KW

KW

KW

OS

OS

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PN

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07-MAY-1999 (first entry)

A murine homologue of human zneurok1 polypeptide.

Human; zneurok1; neurokinin B; prohormone convertase; cell growth;

modulation; inflammation; noinception; emesis; contraction;

hormone secretion; DNA synthesis; inositol phosphate turnover;

arachidonate release; phospholipase-C activation; gastric emptying;

human neutrophil activation; ADCC capability;

superoxide anion production; gene therapy.

Mus sp.

W09855612-A1.

10-DEC-1998.

28-MAY-1998; 98WO-US10842.

02-JUN-1997; 97US-0048290.

(ZYMO) ZYMOGENETICS INC.

Sheppard PO;

WPI; 1999-070268/06.

N-PSDB; AAX15448.

New isolated neurokinin polypeptides, zneurok1 - used to develop

products for modulating e.g. inflammation, noinception, emesis,

muscle contraction, hormone secretion, DNA synthesis or cell growth

Example 1; Page 87; 100pp; English.

The present sequence represents a murine homologue of human zneurok1. The

zneurok1 polypeptide releases a neurokinin B polypeptide in the presence

of a prohormone convertase capable of cleaving dibasic amino

acids. The zneurok1 polypeptides can be used for modulating inflammation,

noinception or emesis. The polypeptides, fragments, fusion proteins,

agonists, antagonists or antibodies may also modulate contraction,

hormone secretion, DNA synthesis or cell growth, inositol phosphate

turnover, arachidonate release, phospholipase-C activation, gastric

emptying, human neutrophil activation or ADCC capability, or superoxide

anion production. The polynucleotides can also be used for gene therapy.

The products can also be used for detection, diagnosis and screening

assays.

Sequence 92 AA;

Query Match 8.3%; Score 10; DB 20; Length 92;

Best Local Similarity 100.0%; Pred. No. 0.025;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDMHDFVFG 88

|||||||

Db 80 krdmhdfvfg 89

RESULT 15

AAW96146

ID AAW96146 standard; Protein; 116 AA.

XX AAW96146;

XX AAW96146;

DT 27-APR-1999 (first entry)

XX Rat preprotachykinin B.

DE Preprotachykinin B; PPT-B; neoplastic disorder;

KW neurological disorder; Alzheimer's disease; amnesia;

KW cerebral neoplasms; dementia; depression; Down's syndrome;

KW Huntington's disease; multiple sclerosis; Parkinson's disease;
KW paranoïd psychoses; schizophrenia; Tourette's disorder; angina;
KW anaphylactic shock; asthma; cardiovascular shock;
XX myocardial infarction; migraine.
OS - Rattus rattus.
XX
XX
PN WO9857986-A2.
XX
PD 23-DEC-1998.
XX
XX
PF 19-JUN-1998; 98WO-US12855.
XX
XX
PR 19-JUN-1997; 97US-0879995.
XX
XX (INCY-) INCYTE PHARM INC.
PA
XX
PI Hillman JJ, Kaser MR, Lal P;
XX
XX WPI; 1999-080948/07.
DR
XX
XX New human preprotachykinin B - useful for treating neurological
PT disorders and cancer
XX
XX
PS Disclosure; Figure 2; 57pp; English.
XX
XX
CC Human preprotachykinin B (AAW96144) (PPT-B) can be used to treat a
CC neurological disorder. Antagonists of PPT-B can also be used in
CC the treatment of neoplastic disorders. Particular neurological,
CC disorders include akathisia, Alzheimer's disease, amnesia,
CC amyotrophic lateral sclerosis, bipolar disorder, catatonia,
CC cerebral neoplasms, dementia, depression, Down's syndrome, tardive
CC dyskinesia, dystonias, Huntington's disease, multiple sclerosis,
CC neurofibromatosis, Parkinson's disease, paranoïd psychoses,
CC schizoprenia, and Tourette's disorder. PPT-B or its agonist can
CC also be used to treat angina, anaphylactic shock, arrhythmias,
CC asthma, cardiovascular shock, Cushing's syndrome, hypertension,
CC hypoglycemia, myocardial infarction, migraine and pheochromocytoma.
XX
XX
SQ Sequence 116 AA;

Query Match 8.3%; Score 10; DB 20; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDMHDFVVG 88
Db 80 krdmhdffvg 89

Search completed: May 3, 2002, 12:28:31
Job time: 223 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 12:26:43 ; Search time 12.76 Seconds
(without alignments) 213.393 Million cell

Title: US-09-852-659-85

Perfect score: 121

Sequence: 1 MRIMLLFTAILAFSLAQSG.....DVNQENVPSFGILKYPPRAE 121

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/pdata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/pdata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/pdata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/pdata/2/1aa/PCRTUS_COMB.pep.*
6: /cgn2_6/pdata/2/1aa/backfiles1.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	66	54.5	122	2	US-08-879-995A-1		Sequence 1, Appli
2	66	54.5	122	3	US-09-213-096-1		Sequence 1, Appli
3	10	8.3	116	2	US-08-879-995A-4		Sequence 4, Appli
4	10	8.3	116	3	US-09-215-096-4		Sequence 4, Appli
5	10	8.3	126	2	US-08-879-995A-3		Sequence 3, Appli
6	10	8.3	126	3	US-09-215-096-3		Sequence 3, Appli
7	8	6.6	10	1	US-07-899-205-3		Sequence 3, Appli
8	8	6.6	10	1	US-08-184-935-10		Sequence 10, Appli
9	8	6.6	10	1	US-08-269-288-4		Sequence 4, Appli
10	8	6.6	10	1	US-08-338-484-3		Sequence 3, Appli
11	8	6.6	10	1	US-08-175-432-3		Sequence 3, Appli
12	8	6.6	10	1	US-08-462-413-4		Sequence 3, Appli
13	8	6.6	10	1	US-08-391-910-4		Sequence 4, Appli
14	8	6.6	10	1	US-08-418-994-4		Sequence 4, Appli
15	8	6.6	10	1	US-08-391-814-4		Sequence 4, Appli
16	8	6.6	10	1	US-08-167-870-3		Sequence 4, Appli
17	8	6.6	10	1	US-08-462-415-4		Sequence 3, Appli
18	8	6.6	10	1	US-08-463-874-4		Sequence 4, Appli
19	8	6.6	10	1	US-08-318-391-4		Sequence 4, Appli
20	8	6.6	10	2	US-08-496-118-3		Sequence 3, Appli
21	8	6.6	10	2	US-07-737-371E-74		Sequence 74, Appli
22	8	6.6	10	4	US-08-257-966-4		Sequence 4, Appli
23	7	5.8	590	1	US-08-221-817-14		Sequence 14, Appli
24	7	5.8	590	1	US-08-454-439-14		Sequence 14, Appli
25	7	5.8	590	4	US-08-464-954A-5		Sequence 5, Appli
26	7	5.8	590	5	PCT-US94-10487-14		Sequence 14, Appli
27	6	5.0	10	2	US-07-737-371E-43		Sequence 43, Appli

101	6	5.0	528	2	US-08-484-956-90	Sequence 90, Appl	174	6	5.0	833	2	US-08-757-653-190	Sequence 190, Appl
102	6	5.0	528	2	US-08-757-653-90	Sequence 90, Appl	175	6	5.0	833	2	US-08-599-491-8	Sequence 8, Appl1
103	6	5.0	548	2	US-08-484-956-86	Sequence 86, Appl	176	6	5.0	833	2	US-08-756-386-8	Sequence 8, Appl1
104	6	5.0	548	2	US-08-757-653-86	Sequence 86, Appl	177	6	5.0	833	2	US-08-823-516-8	Sequence 8, Appl1
105	6	5.0	556	4	US-08-687-590-24	Sequence 24, Appl	178	6	5.0	833	2	US-08-823-516-66	Sequence 66, Appl
106	6	5.0	563	4	US-08-906-743-2	Sequence 2, Appl1	179	6	5.0	833	2	US-08-823-516-69	Sequence 69, Appl
107	6	5.0	576	1	US-08-221-817-13	Sequence 13, Appl	180	6	5.0	833	2	US-08-823-516-71	Sequence 71, Appl
108	6	5.0	576	1	US-08-221-817-22	Sequence 22, Appl	181	6	5.0	833	3	US-08-682-853A-8	Sequence 8, Appl1
109	6	5.0	576	1	US-08-454-439-13	Sequence 13, Appl	182	6	5.0	833	3	US-08-759-038-8	Sequence 8, Appl1
110	6	5.0	576	1	US-08-454-439-22	Sequence 22, Appl	183	6	5.0	833	3	US-08-759-038-107	Sequence 107, App
111	6	5.0	576	1	US-08-464-954A-6	Sequence 6, Appl1	184	6	5.0	833	3	US-08-759-038-130	Sequence 130, App
112	6	5.0	576	5	PCR-US94-10487-13	Sequence 13, Appl	185	6	5.0	833	3	US-08-759-038-132	Sequence 132, App
113	6	5.0	576	5	PCR-US94-10487-22	Sequence 22, Appl	186	6	5.0	833	3	US-08-758-314-8	Sequence 8, Appl1
114	6	5.0	584	1	US-08-426-819A-36	Sequence 36, Appl	187	6	5.0	833	3	US-08-758-314-107	Sequence 107, App
115	6	5.0	622	1	US-08-426-819A-35	Sequence 35, Appl	188	6	5.0	833	3	US-08-758-314-130	Sequence 130, App
116	6	5.0	628	3	US-08-776-271-2	Sequence 2, Appl1	189	6	5.0	833	3	US-08-758-314-132	Sequence 132, App
117	6	5.0	628	4	US-08-213-035-2	Sequence 2, Appl1	190	6	5.0	948	1	US-08-698-551-14	Sequence 14, Appl
118	6	5.0	632	1	US-08-221-817-11	Sequence 11, Appl	191	6	5.0	948	2	US-08-602-228-14	Sequence 14, Appl
119	6	5.0	632	1	US-08-454-439-11	Sequence 11, Appl	192	6	5.0	948	2	US-08-533-901B-14	Sequence 14, Appl
120	6	5.0	632	5	PCR-US94-10487-11	Sequence 11, Appl	193	6	5.0	948	2	US-08-839-032A-14	Sequence 14, Appl
121	6	5.0	695	2	US-08-484-956-87	Sequence 87, Appl	194	6	5.0	948	2	US-08-839-031A-14	Sequence 14, Appl
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123	6	5.0	737	1	US-08-185-432-2	Sequence 2, Appl1	196	6	5.0	1275	3	US-09-120-513-2	Sequence 2, Appl1
124	6	5.0	737	1	US-08-185-432-4	Sequence 4, Appl1	197	6	5.0	1275	4	US-09-450-103-2	Sequence 2, Appl1
125	6	5.0	810	4	US-09-587-856-2	Sequence 2, Appl1	198	6	5.0	7257	3	US-09-335-409-5	Sequence 5, Appl1
126	6	5.0	830	1	US-07-977-434-6	Sequence 6, Appl1	199	5	4.1	5	1	US-08-127-904-1	Sequence 1, Appl1
127	6	5.0	830	1	US-08-458-819-6	Sequence 6, Appl1	200	5	4.1	5	5	PCR-US94-10475-1	Sequence 1, Appl1
128	6	5.0	830	5	PCR-US91-07035-6	Sequence 6, Appl1	201	5	4.1	8	1	US-07-876-280-11	Sequence 11, Appl
129	6	5.0	831	1	US-08-073-384C-5	Sequence 5, Appl1	202	5	4.1	8	1	US-07-968-781A-61	Sequence 61, Appl
130	6	5.0	831	1	US-08-254-359A-5	Sequence 5, Appl1	203	5	4.1	8	1	US-08-158-232-14	Sequence 14, Appl
131	6	5.0	831	1	US-08-483-043-5	Sequence 5, Appl1	204	5	4.1	8	1	US-08-304-626-14	Sequence 14, Appl
132	6	5.0	831	1	US-08-481-238-5	Sequence 5, Appl1	205	5	4.1	8	1	US-08-316-301A-15	Sequence 15, Appl
133	6	5.0	831	2	US-08-471-066B-5	Sequence 5, Appl1	206	5	4.1	8	3	US-08-611-928-14	Sequence 14, Appl
134	6	5.0	831	2	US-08-484-956-5	Sequence 5, Appl1	207	5	4.1	8	4	US-09-076-137-15	Sequence 15, Appl
135	6	5.0	831	2	US-08-757-653-5	Sequence 5, Appl1	208	5	4.1	8	4	US-09-139-802-104	Sequence 104, App
136	6	5.0	831	2	US-08-599-491-5	Sequence 5, Appl1	209	5	4.1	8	5	PCR-US92-03624-15	Sequence 15, Appl
137	6	5.0	831	2	US-08-756-386-5	Sequence 5, Appl1	210	5	4.1	8	2	US-08-599-602-38	Sequence 38, Appl
138	6	5.0	831	2	US-08-623-516-5	Sequence 5, Appl1	211	5	4.1	9	3	US-09-197-816-38	Sequence 38, Appl
139	6	5.0	831	3	US-08-682-853A-5	Sequence 5, Appl1	212	5	4.1	11	4	US-09-196-293-7	Sequence 7, Appl1
140	6	5.0	831	3	US-08-759-038-5	Sequence 5, Appl1	213	5	4.1	11	4	US-08-209-603E-7	Sequence 7, Appl1
141	6	5.0	831	3	US-08-758-314-5	Sequence 5, Appl1	214	5	4.1	11	6	5194592-77	Patent No. 5194592
142	6	5.0	832	1	US-07-977-434-2	Sequence 2, Appl1	215	5	4.1	14	1	US-08-232-453A-40	Sequence 40, Appl
143	6	5.0	832	1	US-08-156-020-2	Sequence 2, Appl1	216	5	4.1	14	1	US-08-232-453A-46	Sequence 46, Appl
144	6	5.0	832	1	US-08-156-020-4	Sequence 4, Appl1	217	5	4.1	14	1	US-08-232-453A-46	Sequence 46, Appl
145	6	5.0	832	1	US-08-156-020-6	Sequence 6, Appl1	218	5	4.1	14	1	US-07-977-696C-39	Sequence 39, Appl
146	6	5.0	832	1	US-08-156-020-8	Sequence 8, Appl1	219	5	4.1	14	1	US-08-129-930B-39	Sequence 39, Appl
147	6	5.0	832	1	US-08-156-020-10	Sequence 10, Appl	220	5	4.1	14	2	US-08-529-190B-76	Sequence 76, Appl
148	6	5.0	832	1	US-08-073-384C-4	Sequence 4, Appl1	221	5	4.1	14	4	US-08-134-346A-26	Sequence 26, Appl
149	6	5.0	832	1	US-08-254-359A-4	Sequence 4, Appl1	222	5	4.1	15	2	US-08-726-306A-55	Sequence 55, Appl
150	6	5.0	832	1	US-08-483-043-4	Sequence 4, Appl1	223	5	4.1	16	2	US-08-434-834-7	Sequence 7, Appl1
151	6	5.0	832	1	US-08-458-819-2	Sequence 2, Appl1	224	5	4.1	17	2	US-08-434-834-6	Sequence 6, Appl1
152	6	5.0	832	1	US-08-481-238-4	Sequence 4, Appl1	225	5	4.1	17	4	US-08-905-223-18	Sequence 18, Appl
153	6	5.0	832	2	US-08-471-066B-4	Sequence 4, Appl1	226	5	4.1	18	1	US-07-855-412B-3	Sequence 3, Appl1
154	6	5.0	832	2	US-08-484-956-4	Sequence 4, Appl1	227	5	4.1	18	2	US-08-308-887A-3	Sequence 3, Appl1
155	6	5.0	832	2	US-08-757-653-4	Sequence 4, Appl1	228	5	4.1	18	3	US-08-881-094-3	Sequence 3, Appl1
156	6	5.0	832	2	US-08-599-491-4	Sequence 4, Appl1	229	5	4.1	18	3	US-08-881-094-9	Sequence 9, Appl1
157	6	5.0	832	2	US-08-756-386-4	Sequence 4, Appl1	230	5	4.1	18	3	US-08-881-094-10	Sequence 10, Appl
158	6	5.0	832	2	US-08-823-516-4	Sequence 4, Appl1	231	5	4.1	19	3	US-08-788-231A-14	Sequence 14, Appl
159	6	5.0	832	3	US-08-682-853A-4	Sequence 4, Appl1	232	5	4.1	20	1	US-08-399-696-79	Sequence 79, Appl
160	6	5.0	832	3	US-08-759-038-4	Sequence 4, Appl1	233	5	4.1	20	3	US-08-837-226-12	Sequence 12, Appl
161	6	5.0	832	3	US-08-758-314-4	Sequence 4, Appl1	234	5	4.1	21	1	US-08-768-269-15	Sequence 15, Appl
162	6	5.0	832	5	PCR-US91-07035-2	Sequence 2, Appl1	235	5	4.1	21	1	US-07-908-455A-6	Sequence 6, Appl1
163	6	5.0	833	1	US-08-073-384C-8	Sequence 8, Appl1	236	5	4.1	21	1	US-07-908-455A-7	Sequence 7, Appl1
164	6	5.0	833	1	US-08-254-359A-8	Sequence 8, Appl1	237	5	4.1	21	1	US-08-434-120-32	Sequence 32, Appl
165	6	5.0	833	1	US-08-483-043-8	Sequence 8, Appl1	238	5	4.1	21	1	US-08-434-120-33	Sequence 33, Appl
166	6	5.0	833	1	US-08-481-238-8	Sequence 8, Appl1	239	5	4.1	21	1	US-08-465-325-33	Sequence 33, Appl
167	6	5.0	833	2	US-08-471-066B-8	Sequence 8, Appl1	240	5	4.1	21	1	US-08-465-325-33	Sequence 33, Appl
168	6	5.0	833	2	US-08-484-956-8	Sequence 8, Appl1	241	5	4.1	21	1	US-08-635-928-24	Sequence 24, Appl
169	6	5.0	833	2	US-08-484-956-85	Sequence 85, Appl	242	5	4.1	21	1	US-08-380-438-3	Sequence 3, Appl1
170	6	5.0	833	2	US-08-757-653-8	Sequence 8, Appl1	243	5	4.1	22	1	US-08-169-948B-30	Sequence 30, Appl
171	6	5.0	833	2	US-08-757-653-85	Sequence 85, Appl	244	5	4.1	22	2	US-08-448-873-30	Sequence 30, Appl
172	6	5.0	833	2	US-08-757-653-168	Sequence 168, App	245	5	4.1	22	2	US-08-448-873-30	Sequence 30, Appl
173	6	5.0	833	2	US-08-757-653-188	Sequence 188, App	246	5	4.1	22	3	US-08-940-095-39	Sequence 39, Appl

247	5	4.1	22	3	US-08-940-095-57	Sequence 57, Appl	320	5	4.1	37	1	US-08-471-675A-25	Sequence 25, Appl
248	5	4.1	22	3	US-08-940-095-134	Sequence 134, Appl	321	5	4.1	37	1	US-08-471-675A-27	Sequence 27, Appl
249	5	4.1	22	3	US-08-940-093-39	Sequence 39, Appl	322	5	4.1	37	2	US-08-259-762-10	Sequence 10, Appl
250	5	4.1	22	3	US-08-940-093-57	Sequence 57, Appl	323	5	4.1	37	2	US-08-259-762-11	Sequence 11, Appl
251	5	4.1	22	3	US-08-940-093-134	Sequence 134, Appl	324	5	4.1	37	2	US-08-892-549-29	Sequence 29, Appl
252	5	4.1	22	3	US-08-940-096-39	Sequence 39, Appl	325	5	4.1	37	2	US-08-892-549-31	Sequence 31, Appl
253	5	4.1	22	3	US-08-940-096-57	Sequence 57, Appl	326	5	4.1	37	3	US-08-302-069A-24	Sequence 24, Appl
254	5	4.1	22	3	US-08-940-096-134	Sequence 134, Appl	327	5	4.1	37	3	US-08-302-069A-26	Sequence 26, Appl
255	5	4.1	22	4	US-09-465-719-39	Sequence 39, Appl	328	5	4.1	40	3	US-08-792-832A-54	Sequence 54, Appl
256	5	4.1	22	4	US-09-465-719-57	Sequence 57, Appl	329	5	4.1	40	3	US-08-792-832A-56	Sequence 56, Appl
257	5	4.1	22	4	US-09-465-719-134	Sequence 134, Appl	330	5	4.1	41	4	US-08-789-333F-27	Sequence 27, Appl
258	5	4.1	22	4	US-08-382-452D-30	Sequence 30, Appl	331	5	4.1	41	4	US-09-169-015-37	Sequence 37, Appl
259	5	4.1	22	4	US-08-112-208C-20	Sequence 20, Appl	332	5	4.1	41	4	US-09-133-944-26	Sequence 26, Appl
260	5	4.1	23	1	US-08-248-819A-22	Sequence 22, Appl	333	5	4.1	42	4	US-09-309-382-12	Sequence 12, Appl
261	5	4.1	23	2	US-08-337-646A-40	Sequence 40, Appl	334	5	4.1	47	2	US-08-935-396-2	Sequence 2, Appl
262	5	4.1	23	2	US-08-856-531-20	Sequence 20, Appl	335	5	4.1	51	1	US-08-905-223-284	Sequence 284, Appl
263	5	4.1	23	2	US-08-856-531-20	Sequence 20, Appl	336	5	4.1	51	2	US-08-346-849-12	Sequence 12, Appl
264	5	4.1	23	4	US-08-927-326-40	Sequence 40, Appl	337	5	4.1	51	2	US-08-293-284A-12	Sequence 12, Appl
265	5	4.1	24	1	US-08-325-071-30	Sequence 30, Appl	338	5	4.1	54	1	US-08-485-455D-39	Sequence 39, Appl
266	5	4.1	24	1	US-08-181-271A-52	Sequence 52, Appl	339	5	4.1	54	2	US-08-482-130C-39	Sequence 39, Appl
267	5	4.1	24	1	US-08-449-315-52	Sequence 52, Appl	340	5	4.1	54	2	US-08-484-211C-39	Sequence 39, Appl
268	5	4.1	24	1	US-08-449-315-52	Sequence 52, Appl	341	5	4.1	54	3	US-08-906-769-39	Sequence 39, Appl
269	5	4.1	24	1	US-08-449-043-52	Sequence 52, Appl	342	5	4.1	54	4	US-08-817-795-39	Sequence 39, Appl
270	5	4.1	24	1	US-08-456-265A-52	Sequence 52, Appl	343	5	4.1	54	4	US-08-485-443B-39	Sequence 39, Appl
271	5	4.1	24	1	US-08-455-416-52	Sequence 52, Appl	344	5	4.1	54	4	US-08-639-075A-39	Sequence 39, Appl
272	5	4.1	24	1	US-08-455-244-52	Sequence 52, Appl	345	5	4.1	54	4	US-09-012-431-39	Sequence 39, Appl
273	5	4.1	24	1	US-08-454-876-52	Sequence 52, Appl	346	5	4.1	54	4	US-09-012-692-39	Sequence 39, Appl
274	5	4.1	24	2	US-08-457-364-52	Sequence 52, Appl	347	5	4.1	54	4	US-08-906-613-39	Sequence 39, Appl
275	5	4.1	24	2	US-08-456-262-52	Sequence 52, Appl	348	5	4.1	54	4	US-08-906-613-39	Sequence 39, Appl
276	5	4.1	24	2	US-08-456-240-52	Sequence 52, Appl	349	5	4.1	54	4	US-08-906-613-39	Sequence 39, Appl
277	5	4.1	24	2	US-08-455-736-52	Sequence 52, Appl	350	5	4.1	54	4	US-08-906-613-39	Sequence 39, Appl
278	5	4.1	24	2	US-08-971-217-52	Sequence 52, Appl	351	5	4.1	56	4	US-08-817-795-39	Sequence 39, Appl
279	5	4.1	24	4	US-08-461-004A-30	Sequence 30, Appl	352	5	4.1	56	4	US-08-817-795-39	Sequence 39, Appl
280	5	4.1	24	4	US-08-350-600-52	Sequence 52, Appl	353	5	4.1	56	4	US-08-817-795-39	Sequence 39, Appl
281	5	4.1	25	1	US-08-172-331B-9	Sequence 9, Appl	354	5	4.1	67	1	US-08-630-524-14	Sequence 14, Appl
282	5	4.1	25	1	US-08-468-709B-13	Sequence 13, Appl	355	5	4.1	67	1	US-07-938-782A-14	Sequence 14, Appl
283	5	4.1	25	1	US-08-468-709B-15	Sequence 15, Appl	356	5	4.1	67	1	US-08-248-839C-159	Sequence 159, Appl
284	5	4.1	25	1	US-08-468-709B-16	Sequence 16, Appl	357	5	4.1	75	2	US-08-905-223-330	Sequence 330, Appl
285	5	4.1	25	2	US-08-241-664B-13	Sequence 13, Appl	358	5	4.1	76	2	US-08-469-537A-38	Sequence 38, Appl
286	5	4.1	25	2	US-08-241-664B-15	Sequence 15, Appl	359	5	4.1	76	2	US-08-469-537A-39	Sequence 39, Appl
287	5	4.1	25	2	US-08-241-664B-16	Sequence 16, Appl	360	5	4.1	77	1	US-08-225-577B-13	Sequence 13, Appl
288	5	4.1	26	1	US-08-281-702A-6	Sequence 6, Appl	361	5	4.1	77	2	US-08-469-537A-41	Sequence 41, Appl
289	5	4.1	26	1	US-08-181-271A-53	Sequence 53, Appl	362	5	4.1	79	4	US-08-469-537A-46	Sequence 46, Appl
290	5	4.1	26	1	US-08-449-315-53	Sequence 53, Appl	363	5	4.1	82	1	US-08-225-577B-12	Sequence 12, Appl
291	5	4.1	26	1	US-08-449-315-53	Sequence 53, Appl	364	5	4.1	84	3	US-08-906-769-99	Sequence 99, Appl
292	5	4.1	26	1	US-08-449-043-53	Sequence 53, Appl	365	5	4.1	84	3	US-08-906-616-99	Sequence 99, Appl
293	5	4.1	26	1	US-08-456-265A-53	Sequence 53, Appl	366	5	4.1	84	4	US-08-817-795-99	Sequence 99, Appl
294	5	4.1	26	1	US-08-455-416-53	Sequence 53, Appl	367	5	4.1	84	4	US-08-639-075A-99	Sequence 99, Appl
295	5	4.1	26	1	US-08-455-244-53	Sequence 53, Appl	368	5	4.1	84	4	US-08-012-431-99	Sequence 99, Appl
296	5	4.1	26	1	US-08-454-876-53	Sequence 53, Appl	369	5	4.1	84	4	US-08-012-692-99	Sequence 99, Appl
297	5	4.1	26	2	US-08-618-917-6	Sequence 6, Appl	370	5	4.1	84	4	US-08-906-613-99	Sequence 99, Appl
298	5	4.1	26	2	US-08-457-364-53	Sequence 53, Appl	371	5	4.1	84	5	PCT-US95-14442A-99	Sequence 99, Appl
299	5	4.1	26	2	US-08-456-262-53	Sequence 53, Appl	372	5	4.1	88	2	US-08-690-011A-11	Sequence 11, Appl
300	5	4.1	26	2	US-08-456-240-53	Sequence 53, Appl	373	5	4.1	90	1	US-08-341-219-24	Sequence 24, Appl
301	5	4.1	26	2	US-08-455-736-53	Sequence 53, Appl	374	5	4.1	90	3	US-08-173-501-4	Sequence 4, Appl
302	5	4.1	26	2	US-08-620-151-101	Sequence 101, Appl	375	5	4.1	90	3	US-08-912-314A-24	Sequence 24, Appl
303	5	4.1	26	2	US-08-971-217-53	Sequence 53, Appl	376	5	4.1	90	4	US-09-420-915-4	Sequence 4, Appl
304	5	4.1	26	2	US-08-389-564B-27	Sequence 27, Appl	377	5	4.1	92	1	US-08-341-219-21	Sequence 21, Appl
305	5	4.1	26	3	US-08-466-047B-27	Sequence 27, Appl	378	5	4.1	92	1	US-08-912-314A-21	Sequence 21, Appl
306	5	4.1	26	3	US-09-350-600-53	Sequence 53, Appl	379	5	4.1	96	2	US-08-739-484-4	Sequence 4, Appl
307	5	4.1	27	2	US-08-310-912A-201	Sequence 201, Appl	380	5	4.1	96	4	US-08-465-343A-11	Sequence 11, Appl
308	5	4.1	27	4	US-09-301-085-201	Sequence 201, Appl	381	5	4.1	98	2	US-08-690-011A-19	Sequence 19, Appl
309	5	4.1	27	5	PCT-US95-04589-201	Sequence 201, Appl	382	5	4.1	98	4	US-09-518-046-17	Sequence 17, Appl
310	5	4.1	31	2	US-08-251-472-9	Sequence 9, Appl	383	5	4.1	100	1	US-08-967-513-3	Sequence 3, Appl
311	5	4.1	31	3	US-09-248-082-9	Sequence 9, Appl	384	5	4.1	100	2	US-08-619-542B-35	Sequence 35, Appl
312	5	4.1	33	6	5169933-45	Patent No. 5169933	385	5	4.1	100	2	US-08-467-822-23	Sequence 23, Appl
313	5	4.1	35	4	US-08-749-066A-6	Sequence 6, Appl	386	5	4.1	100	2	US-08-687-845B-3	Sequence 3, Appl
314	5	4.1	36	1	US-07-929-206-7	Sequence 7, Appl	387	5	4.1	100	4	US-08-432-697-23	Sequence 23, Appl
315	5	4.1	36	1	US-08-313-185-4	Sequence 4, Appl	388	5	4.1	100	4	US-08-466-248-23	Sequence 23, Appl
316	5	4.1	36	2	US-08-459-499-7	Sequence 7, Appl	389	5	4.1	101	1	US-08-271-354-13	Sequence 13, Appl
317	5	4.1	36	3	US-08-082-614A-4	Sequence 4, Appl	390	5	4.1	101	1	US-08-565-861-13	Sequence 13, Appl
318	5	4.1	37	1	US-08-477-727A-103	Sequence 103, Appl	391	5	4.1	101	5	PCT-US94-07658-13	Sequence 13, Appl
319	5	4.1	37	1	US-08-477-727A-105	Sequence 105, Appl	392	5	4.1	102	3	US-08-906-769-125	Sequence 125, Appl

393	4.1	102	3	US-08-906-616-125	Sequence 125, App	466	5	4.1	160	1	US-07-847-010-11	Sequence 11, Appl
394	4.1	102	4	US-08-639-075A-125	Sequence 125, App	467	5	4.1	160	1	US-07-847-010-14	Sequence 17, Appl
395	4.1	102	4	US-09-012-431-125	Sequence 125, App	468	5	4.1	160	1	US-07-847-010-17	Sequence 14, Appl
396	4.1	102	4	US-09-012-692-125	Sequence 125, App	469	5	4.1	160	1	US-07-847-010-20	Sequence 20, Appl
397	4.1	102	4	US-08-906-613-125	Sequence 125, App	470	5	4.1	160	2	US-08-726-306A-35	Sequence 35, Appl
398	4.1	102	4	US-08-619-542B-38	Sequence 38, Appl	471	5	4.1	161	1	US-08-368-832-2	Sequence 2, Appl
399	4.1	103	3	US-08-894-173-76	Sequence 76, Appl	472	5	4.1	161	2	US-08-525-940-2	Sequence 2, Appl
400	4.1	103	3	US-09-398-193-76	Sequence 76, Appl	473	5	4.1	161	2	US-08-976-838-2	Sequence 2, Appl
401	4.1	103	4	US-08-857-076-54	Sequence 54, Appl	474	5	4.1	161	3	US-09-205-264-2	Sequence 2, Appl
402	4.1	105	2	US-08-646-981-3	Sequence 3, Appl	475	5	4.1	162	1	US-07-879-685B-4	Sequence 4, Appl
403	4.1	106	3	US-09-083-351-16	Sequence 16, Appl	476	5	4.1	162	4	US-09-108-020-50	Sequence 50, Appl
404	4.1	106	3	US-09-083-351-17	Sequence 17, Appl	477	5	4.1	165	1	US-08-051-142-2	Sequence 2, Appl
405	4.1	106	3	US-09-083-351-18	Sequence 18, Appl	478	5	4.1	165	2	US-08-602-208-3	Sequence 3, Appl
406	4.1	106	4	US-09-083-352-16	Sequence 16, Appl	479	5	4.1	172	2	US-08-853-659A-46	Sequence 46, Appl
407	4.1	106	4	US-09-083-352-17	Sequence 17, Appl	480	5	4.1	175	1	US-08-010-099-94	Sequence 94, Appl
408	4.1	106	4	US-09-083-352-18	Sequence 18, Appl	481	5	4.1	175	4	US-08-448-716-94	Sequence 94, Appl
409	4.1	106	4	US-08-857-076-37	Sequence 37, Appl	482	5	4.1	175	4	US-09-304-186-94	Sequence 94, Appl
410	4.1	107	2	US-08-810-572A-4	Sequence 4, Appl	483	5	4.1	178	1	US-08-673-269-2	Sequence 2, Appl
411	4.1	108	2	US-08-828-233-3	Sequence 3, Appl	484	5	4.1	179	1	US-08-607-269-27	Sequence 27, Appl
412	4.1	108	2	US-08-828-233-4	Sequence 4, Appl	485	5	4.1	179	5	PCT-US95-04600-27	Sequence 27, Appl
413	4.1	108	3	US-09-205-679-3	Sequence 3, Appl	486	5	4.1	181	1	US-08-471-058-18	Sequence 18, Appl
414	4.1	108	3	US-09-205-679-4	Sequence 4, Appl	487	5	4.1	181	3	US-08-471-057-18	Sequence 18, Appl
415	4.1	109	1	US-08-466-886-24	Sequence 24, Appl	488	5	4.1	188	2	US-08-726-306A-57	Sequence 57, Appl
416	4.1	109	2	US-08-637-759B-261	Sequence 261, App	489	5	4.1	189	1	US-08-152-485-4	Sequence 4, Appl
417	4.1	109	3	US-08-871-355A-261	Sequence 261, App	490	5	4.1	189	1	US-08-463-083-4	Sequence 4, Appl
418	4.1	109	3	US-08-894-173-96	Sequence 96, Appl	491	5	4.1	189	1	US-08-461-359-4	Sequence 4, Appl
419	4.1	109	4	US-09-398-193-96	Sequence 96, Appl	492	5	4.1	189	5	PCT-US94-12904-4	Sequence 4, Appl
420	4.1	109	4	US-08-469-617-24	Sequence 24, Appl	493	5	4.1	193	2	US-08-308-821A-6	Sequence 6, Appl
421	4.1	109	4	US-08-857-076-56	Sequence 56, Appl	494	5	4.1	193	3	US-08-831-627-6	Sequence 6, Appl
422	4.1	109	5	PCT-US95-09589-2	Sequence 2, Appl	495	5	4.1	193	3	US-08-765-381-15	Sequence 15, Appl
423	4.1	109	5	PCT-US95-09589A-2	Sequence 2, Appl	496	5	4.1	193	3	US-08-881-094-1	Sequence 1, Appl
424	4.1	110	3	US-08-516-859A-101	Sequence 101, App	497	5	4.1	194	3	US-08-881-094-17	Sequence 17, Appl
425	4.1	112	2	US-08-739-484-3	Sequence 3, Appl	498	5	4.1	197	4	US-08-804-372A-32	Sequence 32, Appl
426	4.1	114	2	US-08-828-239-1	Sequence 1, Appl	499	5	4.1	200	1	US-07-855-412B-1	Sequence 1, Appl
427	4.1	114	2	US-09-205-679-1	Sequence 1, Appl	500	5	4.1	200	3	US-08-308-887A-1	Sequence 1, Appl
428	4.1	116	2	US-08-846-134-1	Sequence 1, Appl	501	5	4.1	201	3	US-08-881-094-1	Sequence 3, Appl
429	4.1	116	2	US-08-853-659A-42	Sequence 42, Appl	502	5	4.1	201	4	US-08-236-427-3	Sequence 3, Appl
430	4.1	117	3	US-08-234-812-1	Sequence 1, Appl	503	5	4.1	201	4	US-09-220-528-116	Sequence 116, App
431	4.1	117	3	US-08-545-809A-133	Sequence 133, App	504	5	4.1	202	3	US-08-881-094-18	Sequence 18, Appl
432	4.1	117	4	US-09-036-315-6	Sequence 6, Appl	505	5	4.1	203	3	US-08-852-936C-4	Sequence 4, Appl
433	4.1	118	2	US-08-663-809-1	Sequence 1, Appl	506	5	4.1	203	4	US-09-300-328-4	Sequence 4, Appl
434	4.1	118	5	PCT-US93-08435-10	Sequence 10, Appl	507	5	4.1	204	3	US-09-053-197A-29	Sequence 29, Appl
435	4.1	120	1	US-08-542-363-26	Sequence 26, Appl	508	5	4.1	205	1	US-08-155-171B-17	Sequence 17, Appl
436	4.1	120	4	US-09-100-089-26	Sequence 26, Appl	509	5	4.1	205	2	US-08-435-998-17	Sequence 17, Appl
437	4.1	122	1	US-08-266-451B-18	Sequence 18, Appl	510	5	4.1	207	1	US-08-557-917A-2	Sequence 2, Appl
438	4.1	122	2	US-08-748-725-18	Sequence 18, Appl	511	5	4.1	207	4	US-09-084-153-2	Sequence 2, Appl
439	4.1	123	4	US-09-188-930-292	Sequence 292, App	512	5	4.1	207	4	US-08-309-512-4	Sequence 4, Appl
440	4.1	126	6	5268359-5	Patent No. 5268359	513	5	4.1	208	1	PCT-US92-08756A-4	Sequence 4, Appl
441	4.1	127	2	US-08-637-759B-334	Sequence 334, App	514	5	4.1	208	5	US-07-667-276A-2	Sequence 2, Appl
442	4.1	127	3	US-08-871-355A-334	Sequence 334, App	515	5	4.1	210	4	US-08-617-785-16	Sequence 16, Appl
443	4.1	130	6	5268359-2	Patent No. 5268359	516	5	4.1	210	4	US-08-155-171B-16	Sequence 16, Appl
444	4.1	137	1	US-08-468-709B-4	Sequence 4, Appl	517	5	4.1	214	2	US-08-435-998-16	Sequence 16, Appl
445	4.1	137	1	US-08-468-709B-11	Sequence 11, Appl	518	5	4.1	214	2	US-08-506-553C-23	Sequence 23, Appl
446	4.1	137	2	US-08-241-664B-4	Sequence 4, Appl	519	5	4.1	216	3	US-08-470-261-2	Sequence 2, Appl
447	4.1	137	2	US-08-241-664B-11	Sequence 11, Appl	520	5	4.1	219	3	US-08-916-989B-2	Sequence 2, Appl
448	4.1	137	4	US-09-383-586-37	Sequence 37, Appl	521	5	4.1	219	5	PCT-US94-13187-2	Sequence 2, Appl
449	4.1	137	4	PCT-US93-03936-4	Sequence 4, Appl	522	5	4.1	219	5	US-08-297-431B-31	Sequence 31, Appl
450	4.1	144	4	US-09-319-989-4	Sequence 4, Appl	523	5	4.1	220	4	US-08-884-077-2	Sequence 2, Appl
451	4.1	146	4	US-08-792-013-7	Sequence 7, Appl	524	5	4.1	220	4	US-08-297-431B-2	Sequence 2, Appl
452	4.1	147	1	US-08-171-385-5	Sequence 5, Appl	525	5	4.1	221	4	US-08-297-431B-4	Sequence 4, Appl
453	4.1	147	2	US-08-949-584A-2	Sequence 2, Appl	526	5	4.1	221	4	US-08-297-431B-6	Sequence 6, Appl
454	4.1	147	3	US-08-946-329A-59	Sequence 59, Appl	527	5	4.1	221	4	US-08-297-431B-8	Sequence 8, Appl
455	4.1	147	3	US-08-361-441B-5	Sequence 5, Appl	528	5	4.1	221	4	US-08-297-431B-10	Sequence 10, Appl
456	4.1	147	3	US-08-361-441B-42	Sequence 42, Appl	529	5	4.1	221	4	US-08-297-431B-12	Sequence 12, Appl
457	4.1	147	4	US-09-049-672A-27	Sequence 27, Appl	530	5	4.1	221	4	US-08-297-431B-14	Sequence 14, Appl
458	4.1	147	4	US-08-792-013-4	Sequence 4, Appl	531	5	4.1	221	4	US-08-297-431B-16	Sequence 16, Appl
459	4.1	147	4	US-08-792-013-6	Sequence 6, Appl	532	5	4.1	221	4	US-08-297-431B-18	Sequence 18, Appl
460	4.1	147	4	US-09-239-861-2	Sequence 2, Appl	533	5	4.1	221	4	US-08-297-431B-20	Sequence 20, Appl
461	4.1	150	4	US-09-049-672A-3	Sequence 3, Appl	534	5	4.1	221	4	US-08-297-431B-32	Sequence 32, Appl
462	4.1	154	2	US-08-756-749C-3	Sequence 3, Appl	535	5	4.1	221	2	US-08-756-771-3	Sequence 3, Appl
463	4.1	156	2	US-08-777-321A-3	Sequence 3, Appl	536	5	4.1	222	2	US-08-756-771-4	Sequence 4, Appl
464	4.1	158	1	US-08-229-393-2	Sequence 2, Appl	537	5	4.1	222	2	US-08-446-875-14	Sequence 14, Appl
465	4.1	160	1	US-07-847-010-3	Sequence 3, Appl	538	5	4.1	222	2		

539	4.1	222	2	US-09-096-571-3	Sequence 3, Appl	612	5	4.1	274	2	US-08-701-191A-33	Sequence 33, Appl
540	4.1	222	2	US-09-096-571-4	Sequence 4, Appl	613	5	4.1	275	2	US-08-701-191A-38	Sequence 38, Appl
541	4.1	222	4	US-09-309-320-3	Sequence 3, Appl	614	5	4.1	275	2	US-07-857-224B-71	Sequence 71, Appl
542	4.1	222	4	US-09-309-320-4	Sequence 4, Appl	615	5	4.1	276	2	US-08-751-233A-4	Sequence 4, Appl
543	4.1	223	1	US-08-430-633-1	Sequence 1, Appl	616	5	4.1	276	3	US-08-506-553C-26	Sequence 26, Appl
544	4.1	223	2	US-08-936-854-1	Sequence 1, Appl	617	5	4.1	277	5	PCT-US96-10521-8	Sequence 8, Appl
545	4.1	225	1	US-08-360-657-8	Sequence 8, Appl	618	5	4.1	278	1	US-08-258-261B-20	Sequence 20, Appl
546	4.1	226	3	US-09-176-673-3	Sequence 3, Appl	619	5	4.1	278	1	US-08-456-837-20	Sequence 20, Appl
547	4.1	226	4	US-08-679-493A-23	Sequence 23, Appl	620	5	4.1	278	1	US-08-457-342-20	Sequence 20, Appl
548	4.1	227	1	US-08-360-103A-2	Sequence 2, Appl	621	5	4.1	278	1	US-08-457-646A-20	Sequence 20, Appl
549	4.1	229	1	US-08-287-959-7	Sequence 7, Appl	622	5	4.1	278	1	US-08-458-076A-20	Sequence 20, Appl
550	4.1	231	4	US-09-370-098-4	Sequence 4, Appl	623	5	4.1	278	1	US-08-457-335A-20	Sequence 20, Appl
551	4.1	233	4	US-08-438-745-15	Sequence 15, Appl	624	5	4.1	278	1	US-08-729-214-20	Sequence 20, Appl
552	4.1	233	4	US-08-438-745-17	Sequence 17, Appl	625	5	4.1	278	3	US-09-028-934-20	Sequence 20, Appl
553	4.1	233	4	US-09-219-019-13	Sequence 13, Appl	626	5	4.1	278	4	US-09-060-410-17	Sequence 17, Appl
554	4.1	233	4	US-09-219-019-17	Sequence 17, Appl	627	5	4.1	278	4	US-08-557-614-2	Sequence 2, Appl
555	4.1	233	5	PCT-US94-05669A-15	Sequence 15, Appl	628	5	4.1	278	4	US-08-557-614-23	Sequence 23, Appl
556	4.1	233	5	PCT-US94-05669A-17	Sequence 17, Appl	629	5	4.1	280	4	US-09-383-586-18	Sequence 18, Appl
557	4.1	235	4	US-08-438-745-13	Sequence 13, Appl	630	5	4.1	283	4	US-09-135-021-6	Sequence 6, Appl
558	4.1	235	4	US-09-219-019-13	Sequence 13, Appl	631	5	4.1	284	2	US-08-751-233A-6	Sequence 6, Appl
559	4.1	235	4	US-09-244-314-4	Sequence 4, Appl	632	5	4.1	284	2	US-08-751-233A-8	Sequence 8, Appl
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561	4.1	235	5	PCT-US96-10521-5	Sequence 5, Appl	634	5	4.1	291	2	US-09-113-788-5	Sequence 5, Appl
562	4.1	246	1	US-07-887-072B-4	Sequence 4, Appl	635	5	4.1	291	4	US-09-328-869-2	Sequence 2, Appl
563	4.1	246	1	US-08-466-444-4	Sequence 4, Appl	636	5	4.1	291	4	US-09-105-697-4	Sequence 4, Appl
564	4.1	249	2	US-08-685-992-29	Sequence 29, Appl	637	5	4.1	291	4	US-09-105-697-6	Sequence 6, Appl
565	4.1	249	2	US-09-144-925-29	Sequence 29, Appl	638	5	4.1	291	4	US-09-105-697-6	Sequence 6, Appl
566	4.1	252	1	US-07-717-332D-2	Sequence 2, Appl	639	5	4.1	291	4	US-09-111-470-5	Sequence 5, Appl
567	4.1	252	1	US-08-411-777-8	Sequence 8, Appl	640	5	4.1	291	4	US-09-629-774A-2	Sequence 2, Appl
568	4.1	252	2	US-08-853-659A-43	Sequence 43, Appl	641	5	4.1	292	1	US-08-769-309A-3	Sequence 3, Appl
569	4.1	252	3	US-09-057-088-8	Sequence 8, Appl	642	5	4.1	292	2	US-08-688-342-4	Sequence 4, Appl
570	4.1	255	5	PCT-US96-01314-54	Sequence 54, Appl	643	5	4.1	292	2	US-09-113-788-4	Sequence 4, Appl
571	4.1	256	3	US-09-035-706-4	Sequence 4, Appl	644	5	4.1	292	3	US-08-994-570-3	Sequence 3, Appl
572	4.1	256	3	US-08-955-841-4	Sequence 4, Appl	645	5	4.1	293	2	US-08-701-191A-26	Sequence 26, Appl
573	4.1	256	5	PCT-US96-01314-55	Sequence 55, Appl	646	5	4.1	293	2	US-08-610-572A-2	Sequence 2, Appl
574	4.1	257	1	US-08-618-164-2	Sequence 2, Appl	647	5	4.1	293	3	US-09-276-873-2	Sequence 2, Appl
575	4.1	258	3	US-07-857-224B-5	Sequence 3, Appl	648	5	4.1	293	4	US-08-438-745-4	Sequence 4, Appl
576	4.1	258	3	US-09-035-706-3	Sequence 3, Appl	649	5	4.1	293	4	US-08-438-745-6	Sequence 6, Appl
577	4.1	258	3	US-08-955-841-3	Sequence 3, Appl	650	5	4.1	293	4	US-09-219-019-4	Sequence 4, Appl
578	4.1	259	2	US-07-857-224B-49	Sequence 49, Appl	651	5	4.1	293	4	US-09-219-019-6	Sequence 6, Appl
579	4.1	259	2	US-07-857-224B-50	Sequence 50, Appl	652	5	4.1	293	5	PCT-US94-05669A-4	Sequence 4, Appl
580	4.1	259	2	US-07-857-224B-51	Sequence 51, Appl	653	5	4.1	293	5	PCT-US94-05669A-6	Sequence 6, Appl
581	4.1	259	2	US-07-857-224B-52	Sequence 52, Appl	654	5	4.1	294	4	US-09-518-046-4	Sequence 4, Appl
582	4.1	259	2	US-07-857-224B-54	Sequence 54, Appl	655	5	4.1	299	4	US-09-352-990-22	Sequence 22, Appl
583	4.1	259	2	US-07-857-224B-55	Sequence 55, Appl	656	5	4.1	300	1	US-07-640-029-5	Sequence 5, Appl
584	4.1	259	2	US-07-857-224B-56	Sequence 56, Appl	657	5	4.1	300	2	US-08-487-031-2	Sequence 2, Appl
585	4.1	260	2	US-07-857-224B-6	Sequence 6, Appl	658	5	4.1	300	3	US-08-473-034-2	Sequence 2, Appl
586	4.1	260	2	US-07-857-224B-53	Sequence 53, Appl	659	5	4.1	302	1	US-08-439-992A-5	Sequence 5, Appl
587	4.1	260	5	PCT-US96-03916-9	Sequence 9, Appl	660	5	4.1	302	1	US-07-640-029-6	Sequence 6, Appl
588	4.1	261	2	US-07-857-224B-22	Sequence 22, Appl	661	5	4.1	302	1	US-07-921-807B-7	Sequence 7, Appl
589	4.1	261	3	US-09-329-418-6	Sequence 6, Appl	662	5	4.1	302	1	US-07-921-807B-8	Sequence 8, Appl
590	4.1	261	4	US-09-531-914-6	Sequence 6, Appl	663	5	4.1	302	1	US-08-441-944A-7	Sequence 7, Appl
591	4.1	262	1	US-08-397-633A-73	Sequence 73, Appl	664	5	4.1	302	1	US-08-441-944A-8	Sequence 8, Appl
592	4.1	262	2	US-07-857-224B-57	Sequence 57, Appl	665	5	4.1	302	2	US-08-439-992A-6	Sequence 6, Appl
593	4.1	262	2	US-07-857-224B-62	Sequence 62, Appl	666	5	4.1	304	2	US-08-487-031-5	Sequence 5, Appl
594	4.1	262	2	US-07-857-224B-63	Sequence 63, Appl	667	5	4.1	304	3	US-08-473-034-5	Sequence 5, Appl
595	4.1	262	2	US-07-857-224B-64	Sequence 64, Appl	668	5	4.1	305	2	US-08-853-659A-47	Sequence 47, Appl
596	4.1	262	4	US-09-363-189B-6	Sequence 6, Appl	669	5	4.1	306	1	US-08-368-852-13	Sequence 13, Appl
597	4.1	264	2	US-07-857-224B-34	Sequence 34, Appl	670	5	4.1	306	2	US-08-525-940-13	Sequence 13, Appl
598	4.1	264	3	US-08-969-644-12	Sequence 12, Appl	671	5	4.1	307	4	US-08-976-838-13	Sequence 13, Appl
599	4.1	264	3	US-08-444-189-12	Sequence 12, Appl	672	5	4.1	307	4	US-09-049-672A-9	Sequence 9, Appl
600	4.1	264	4	US-08-465-465-2	Sequence 2, Appl	673	5	4.1	309	2	US-08-701-191A-9	Sequence 9, Appl
601	4.1	264	4	US-08-468-544-12	Sequence 12, Appl	674	5	4.1	312	3	US-08-258-287B-55	Sequence 55, Appl
602	4.1	268	1	US-08-015-973-7	Sequence 7, Appl	675	5	4.1	312	3	US-08-368-704C-53	Sequence 53, Appl
603	4.1	268	2	US-08-448-164-7	Sequence 7, Appl	676	5	4.1	312	4	US-08-460-900C-14	Sequence 14, Appl
604	4.1	268	2	US-08-081-929-7	Sequence 7, Appl	677	5	4.1	312	4	US-08-674-509B-14	Sequence 14, Appl
605	4.1	269	2	US-08-701-191A-35	Sequence 35, Appl	678	5	4.1	312	4	US-08-954-698-14	Sequence 14, Appl
606	4.1	270	2	US-07-857-224B-76	Sequence 76, Appl	679	5	4.1	313	2	US-08-356-060A-14	Sequence 14, Appl
607	4.1	271	2	US-07-857-224B-46	Sequence 46, Appl	680	5	4.1	313	2	US-08-446-806-1	Sequence 1, Appl
608	4.1	271	6	5175255-1	Patent No. 5175255	681	5	4.1	314	4	US-09-385-028-6	Sequence 6, Appl
609	4.1	273	2	US-08-701-191A-32	Sequence 32, Appl	682	5	4.1	316	4	US-09-111-470-4	Sequence 4, Appl
610	4.1	274	2	US-08-469-537A-55	Sequence 55, Appl	683	5	4.1	322	2	US-08-353-476-63	Sequence 63, Appl
611	4.1	274	2			684	5	4.1	323	1	US-07-913-107-2	Sequence 2, Appl

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686	5	4.1	323	1	US-08-281-248-2	Sequence 2, Appll	759	5	4.1	361	1	US-08-457-335A-3	Sequence 3, Appll
687	5	4.1	323	1	US-08-838-543-4	Sequence 4, Appll	760	5	4.1	361	1	US-08-729-214-3	Sequence 3, Appll
688	5	4.1	323	5	PCT-US93-06421-1	Sequence 1, Appll	761	5	4.1	361	3	US-09-028-934-3	Sequence 3, Appll
689	5	4.1	325	2	US-08-353-476-64	Sequence 64, Appll	762	5	4.1	361	3	US-09-108-020-47	Sequence 47, Appll
690	5	4.1	325	4	US-09-108-020-49	Sequence 49, Appll	763	5	4.1	363	1	US-07-681-704A-2	Sequence 2, Appll
691	5	4.1	325	4	US-09-041-886-33	Sequence 33, Appll	764	5	4.1	363	3	US-09-068-109-2	Sequence 2, Appll
692	5	4.1	327	3	US-08-513-974B-372	Sequence 372, App	765	5	4.1	363	3	US-09-082-089-5	Sequence 5, Appll
693	5	4.1	328	3	US-08-513-974B-39	Sequence 39, Appll	766	5	4.1	363	4	US-09-108-020-44	Sequence 44, Appll
694	5	4.1	328	3	US-08-513-974B-371	Sequence 371, App	767	5	4.1	366	3	US-09-176-657-2	Sequence 2, Appll
695	5	4.1	329	1	US-08-225-477B-3	Sequence 3, Appll	768	5	4.1	366	3	US-08-746-883-6	Sequence 6, Appll
696	5	4.1	329	5	PCT-US95-04353-3	Sequence 3, Appll	769	5	4.1	366	4	US-09-108-020-46	Sequence 46, Appll
697	5	4.1	330	1	US-08-118-270-21	Sequence 21, Appll	770	5	4.1	367	2	US-08-896-320-1	Sequence 1, Appll
698	5	4.1	330	2	US-08-487-031-10	Sequence 10, Appll	771	5	4.1	367	2	US-08-896-320-3	Sequence 3, Appll
699	5	4.1	330	3	US-08-473-034-10	Sequence 10, Appll	772	5	4.1	368	2	US-08-896-320-4	Sequence 4, Appll
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701	5	4.1	330	5	PCT-US93-08528-21	Sequence 21, Appll	774	5	4.1	370	2	US-08-837-593-7	Sequence 7, Appll
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712	5	4.1	333	5	PCT-US95-08812-4	Sequence 4, Appll	785	5	4.1	372	4	US-08-913-441B-30	Sequence 30, Appll
713	5	4.1	334	2	US-08-665-647-3	Sequence 3, Appll	786	5	4.1	372	4	US-08-430-286A-6	Sequence 6, Appll
714	5	4.1	336	1	US-08-436-044-2	Sequence 2, Appll	787	5	4.1	375	1	US-08-464-523B-22	Sequence 22, Appll
715	5	4.1	336	2	US-08-784-651-4	Sequence 2, Appll	788	5	4.1	375	2	US-08-446-875-8	Sequence 8, Appll
716	5	4.1	336	2	US-08-436-054-2	Sequence 2, Appll	789	5	4.1	375	2	US-08-102-385G-8	Sequence 8, Appll
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ALIGNMENTS

RESULT 1
US-08-879-995A-1
; Sequence 1, Application US/08879995A
; Patent No. 5985606
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/879,995A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:

; LIBRARY: BRAITUT03
; CLONE: 2109906
; US-08-879-995A-1

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Best Local Similarity 100.0%; Pred. No. 1.le-58;
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Db 61 LKALSQ 66

RESULT 2
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; Sequence 1, Application US/09215096
; Patent No. 6008194
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
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; US-09-215-096-1

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RESULT 3
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; Sequence 4, Application US/08879995A
; Patent No. 5985606
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/879,995A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 205725
US-08-879-995A-4

Query Match 8.3%; Score 10; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 79 KRDMHDFVVG 88
|||||
Db 80 KRDMHDFVVG 89

RESULT 4
US-09-215-096-4
; Sequence 4, Application US/09215096
; Patent No. 6008194
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.

; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 205725
US-09-215-096-4
Query Match 8.3%; Score 10; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 79 KRDMHDFVVG 88
|||||
Db 80 KRDMHDFVVG 89
RESULT 5
US-08-879-995A-3
; Sequence 3, Application US/08879995A
; Patent No. 5985606
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/879,995A
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0326 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 163590
US-08-879-995A-3

Query Match 8.3%; Score 10; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDHDFVVG 88
|||||
DB 84 KRDHDFVVG 93

RESULT 6
US-09-215-096-3
Sequence 3, Application US/09215096
Patent No. 6008194
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,096
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0326 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 163590
US-09-215-096-3

Query Match 8.3%; Score 10; DB 3; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDHDFVVG 88
|||||
DB 84 KRDHDFVVG 93

RESULT 7
US-07-899-205-3
Sequence 3, Application US/07899205
Patent No. 5288730
GENERAL INFORMATION:
APPLICANT: Baker, Raymond
APPLICANT: Teall, Martin R.
APPLICANT: Swain, Christopher J.
APPLICANT: Williams, Brian J.
TITLE OF INVENTION: AZABICYCLIC COMPOUNDS PHARMACEUTICAL
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/899,205
FILING DATE: 19920616
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Polk, Manfred
REGISTRATION NUMBER: 27,102
REFERENCE/DOCKET NUMBER: T-1106
TELEPHONE: (908) 594-4285
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-899-205-3

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 DMHDFVVG 88
|||||
DB 1 DMHDFVVG 8

RESULT 8
US-08-184-935-10
; Sequence 10, Application US/08184935
; Patent No. 5476770
; GENERAL INFORMATION:
; APPLICANT: PRADELLES, PHILIPPE
; TITLE OF INVENTION: IMMUNOMETRIC DETERMINATION OF AN ANTIGEN
; TITLE OF INVENTION: OR HAPTEN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,935
; FILING DATE: 24-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5476770man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 846-286-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /note= "C-terminal amide"
US-08-184-935-10

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 DMHDFVVG 88
Db 1 DMHDFVVG 8
|||||||

RESULT 9
US-08-269-288-4
; Sequence 4, Application US/08269288
; Patent No. 5491140
; GENERAL INFORMATION:
; APPLICANT: Bruns, Robert F.
; APPLICANT: Gehlert, Donald R.
; APPLICANT: Howbert, James J.
; APPLICANT: Lunn, William H.W.
; TITLE OF INVENTION: NAPHTHYL TACHYKININ RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/1104
; CITY: Indianapolis
; STATE: Indiana

COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/269,288
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9715
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-269-288-4

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 DMHDFVVG 88
Db 1 DMHDFVVG 8
|||||||

RESULT 10
US-08-338-484-3
; Sequence 3, Application US/08338484
; Patent No. 5494926
; GENERAL INFORMATION:
; APPLICANT: Owens, Andrew P.
; APPLICANT: Teall, Martin R.
; APPLICANT: Williams, Brian J.
; TITLE OF INVENTION: 2/3-(HETEROCYCLIC ALKYL
; TITLE OF INVENTION: AMINO)-1-(SUBSTITUTED PHENYL-METHOXY)-ETHANES/PROPANES AS
; TITLE OF INVENTION: TACHYKININ RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Robert J. No. 5494926th
; STREET: 126 E. Lincoln Ave., P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,484
FILING DATE: 18-NOV-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5494926th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-338-484-3

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098; 0; Indels 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 81 DMHDFVVG 88
|||||
Db 1 DMHDFVVG 8

RESULT 11
US-08-175-432-3
Sequence 3, Application US/08175432
Patent No. 5495047
GENERAL INFORMATION:
APPLICANT: Saari, Walfred S.
APPLICANT: Van Niel, Monique B.
APPLICANT: Williams, Brian J.
TITLE OF INVENTION: FUSED TRICYCLIC COMPOUNDS,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR USE
TITLE OF INVENTION: IN THERAPY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: NORTH, ROBERT J.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/175,432
FILING DATE: 07-JAN-1994
CLASSIFICATION: 560
ATTORNEY/AGENT INFORMATION:
NAME: No. 5495047th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1152Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-175-432-3

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098; 0; Indels 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 81 DMHDFVVG 88
|||||
Db 1 DMHDFVVG 8

RESULT 12
US-08-462-413-4
Sequence 4, Application US/08462413
Patent No. 5530009
GENERAL INFORMATION:
APPLICANT: Cho, Sung Y.
APPLICANT: Copp, James D.
APPLICANT: Ginah, Francis O.
APPLICANT: Hansen, Guy J.
APPLICANT: Hipskind, Phillip A.
APPLICANT: Huff, Bret E.
APPLICANT: Martinelli, Michael J.
APPLICANT: Staszak, Michael A.
APPLICANT: Sharp-Taylor, Roger W.
TITLE OF INVENTION: PROCESS FOR PREPARING NON-PEPTIDYL
TITLE OF INVENTION: TACHYKININ RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/462,413
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/271,708
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9475
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-462-413-4

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098; 0; Indels 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 81 DMHDFVVG 88
|||||
Db 1 DMHDFVVG 8

RESULT 13
US-08-391-910-4
Sequence 4, Application US/08391910
Patent No. 5563133
GENERAL INFORMATION:
APPLICANT: Hipskind, Phillip A.
TITLE OF INVENTION: HEXAMETHYLENEIMINYL TACHYKININ RECEPTOR
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9979
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-391-910-4

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 DMHDFVVG 88
Db 1 DMHDFVVG 8

RESULT 14
US-08-418-994-4
Sequence 4, Application US/08418994
Patent No. 555568
GENERAL INFORMATION:
APPLICANT: Cho, Sung-Yong S.
APPLICANT: Hipskind, Philip A.
APPLICANT: Howbert, J. J.
APPLICANT: Muehl, Brian S.
APPLICANT: Nixon, James A.
TITLE OF INVENTION: 2-ACYLAMINOPROPANAMIDES AS TACHYKININ
RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808

REFERENCE/DOCKET NUMBER: X-8252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-418-994-4

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 DMHDFVVG 88
Db 1 DMHDFVVG 8

RESULT 15
US-08-391-814-4
Sequence 4, Application US/08391814
Patent No. 5607947
GENERAL INFORMATION:
APPLICANT: Hipskind, Philip A.
TITLE OF INVENTION: PYRROLIDINYL TACHYKININ RECEPTOR
ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,814
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-391-814-4

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 DMHDFVVG 88
Db 1 DMHDFVVG 8

Search completed: May 3, 2002, 12:28:47
Job time: 124 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 12:27:04 ; Search time 14.49 Seconds
(without alignments)
636.102 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 121
Sequence: 1 MRIMLLFAILAFSLAQSFQ.....DVNQENVPSFGILKYPPRAE 121

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_68.*

- 1: Pirl.*
- 2: Pirl2.*
- 3: Pirl3.*
- 4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	8.3	116	2 A43779	neurokinin B precu
2	10	8.3	116	2 I65342	tachykinin B precu
3	10	8.3	126	2 A25905	tachykinin B precu
4	8	6.6	10	1 SPGKX	neuromedin K - pig
5	8	6.6	812	2 E75338	DNA gyrase, subuni
6	7	5.8	143	2 S75133	hypothetical prote
7	7	5.8	310	2 H70733	hypothetical prote
8	7	5.8	366	2 T50468	probable maturase
9	7	5.8	377	2 B82846	succinyl-diaminopi
10	7	5.8	394	2 E75439	conserved hypothet
11	7	5.8	475	2 C81351	probable UDP-N-ace
12	7	5.8	493	2 E96664	hypothetical prote
13	7	5.8	496	2 C83122	probable aldehyde
14	7	5.8	534	2 D83775	hypothetical prote
15	7	5.8	590	1 A54372	G protein-coupled
16	7	5.8	590	2 A48277	G protein-coupled
17	7	5.8	648	1 A64167	cytochrome c-type
18	7	5.8	702	2 A86383	hypothetical prote
19	7	5.8	712	2 T33231	hypothetical prote
20	7	5.8	1038	2 T51518	ubiquitin-fusion d
21	7	5.8	1058	2 T50496	hypothetical prote
22	7	5.8	1516	2 F84919	glutathione-conjug
23	6	5.0	20	2 FC2084	serine proteinase
24	6	5.0	35	2 PS0439	potassium channel
25	6	5.0	72	1 C24033	small acid-soluble
26	6	5.0	73	1 B24543	small acid-soluble
27	6	5.0	77	2 E71367	hypothetical prote
28	6	5.0	80	2 S78706	protein YER058c-a
29	6	5.0	84	2 S48815	hypothetical prote

30	6	5.0	87	2 T18152	hypothetical prote
31	6	5.0	97	2 T25342	hypothetical prote
32	6	5.0	98	2 D70069	hypothetical prote
33	6	5.0	104	2 S56789	hypothetical prote
34	6	5.0	105	2 G71102	hypothetical prote
35	6	5.0	105	2 B82149	conserved hypothet
36	6	5.0	108	1 WWVP5	nucleic acid-bindi
37	6	5.0	108	2 S12976	12K protein - pota
38	6	5.0	109	2 S34135	hypothetical prote
39	6	5.0	110	2 S12028	hypothetical prote
40	6	5.0	110	2 H64512	hypothetical prote
41	6	5.0	118	2 S72690	probable membrane
42	6	5.0	130	2 C55546	flagellar protein
43	6	5.0	130	2 F64950	flagellar protein
44	6	5.0	130	2 H85800	flagellar protein
45	6	5.0	132	2 S14977	glycine-rich prote
46	6	5.0	142	2 A49296	hemoglobin alpha-B
47	6	5.0	143	2 T13179	hypothetical prote
48	6	5.0	152	1 MYPN	myoglobin - empero
49	6	5.0	152	2 H72578	hypothetical prote
50	6	5.0	153	1 MYSLG	myoglobin - gray s
51	6	5.0	153	1 MYSLH	myoglobin [validat
52	6	5.0	153	1 MYWHP	myoglobin [validat
53	6	5.0	153	2 JN0344	myoglobin - Baikal
54	6	5.0	153	2 A72483	hypothetical prote
55	6	5.0	154	2 S48026	ribosomal protein
56	6	5.0	155	2 S30953	gene 5 protein - M
57	6	5.0	156	2 I37222	dimeric cap bindin
58	6	5.0	156	2 S60109	nuclear cap bindin
59	6	5.0	160	2 A71300	conserved hypothet
60	6	5.0	162	2 D64471	hypothetical prote
61	6	5.0	168	2 T52480	cytochrome-c oxida
62	6	5.0	169	2 F69072	hypothetical prote
63	6	5.0	173	2 S52132	t-complex-type mol
64	6	5.0	173	2 T19290	hypothetical prote
65	6	5.0	177	2 F69365	conserved hypothet
66	6	5.0	179	2 S54186	outer surface prot
67	6	5.0	179	2 S54187	outer surface prot
68	6	5.0	179	2 S54188	outer surface prot
69	6	5.0	180	2 S54191	outer surface prot
70	6	5.0	182	2 E71528	probable transcrip
71	6	5.0	183	1 QOBPCL	git protein - phag
72	6	5.0	191	2 H72767	hypothetical prote
73	6	5.0	191	2 E84740	hypothetical prote
74	6	5.0	191	2 F84522	probable prolina-r
75	6	5.0	193	2 S70265	outer surface prot
76	6	5.0	193	2 C84405	hypothetical prote
77	6	5.0	193	2 T30325	hypothetical prote
78	6	5.0	195	2 T48864	rac-like protein A
79	6	5.0	196	2 T48865	GTP-binding protei
80	6	5.0	197	2 A47525	GTP-binding protei
81	6	5.0	197	2 T04705	rac-like GTP bindi
82	6	5.0	197	2 T08857	probable GTP-bindi
83	6	5.0	197	2 T45761	rac-like GTP bindi
84	6	5.0	198	2 T51962	Rac-like GTP bindi
85	6	5.0	199	2 T01596	GTP-binding protei
86	6	5.0	199	2 A82721	conserved hypothet
87	6	5.0	205	2 T46434	hypothetical prote
88	6	5.0	208	2 C82927	hypothetical prote
89	6	5.0	209	2 E64791	enterobactin synth
90	6	5.0	209	2 A85557	enterobactin synth
91	6	5.0	211	2 T40278	outer surface prot
92	6	5.0	212	2 S13293	KDEL receptor - hu
93	6	5.0	212	2 A44394	KDEL receptor - bo
94	6	5.0	212	2 S69921	outer surface prot
95	6	5.0	212	2 S20543	outer surface prot
96	6	5.0	218	2 T01104	disease resistance
97	6	5.0	219	2 H96608	hypothetical prote
98	6	5.0	221	2 D83471	hypothetical prote
99	6	5.0	223	2 E69181	conserved hypothet
100	6	5.0	227	2 D84381	hypothetical prote
101	6	5.0	228	2 C83663	hypothetical prote
102	6	5.0	231	2 S75387	hypothetical prote

103	6	5.0	231	2	S15139	23S rRNA intron 1	176	6	5.0	354	2	T24094	hypothetical prote
104	6	5.0	232	2	A83208	hypothetical prote	177	6	5.0	355	2	T52177	root hairless prot
105	6	5.0	238	2	F72522	hypothetical prote	178	6	5.0	357	2	B81396	probable aminotran
106	6	5.0	239	2	S52823	hypothetical prote	179	6	5.0	359	2	E83251	probable aminotran
107	6	5.0	239	2	T01463	hypothetical prote	180	6	5.0	359	2	S44425	angiotensin II rec
108	6	5.0	240	1	W2BE39	gene 39 protein -	181	6	5.0	359	2	JH0621	angiotensin II rec
109	6	5.0	240	2	T24957	hypothetical prote	182	6	5.0	359	2	JC2134	angiotensin II rec
110	6	5.0	240	2	B82833	conserved hypotet	183	6	5.0	359	2	A75438	recF protein - Def
111	6	5.0	241	2	T38217	probable transcrip	184	6	5.0	360	2	C64628	lipid A disacchari
112	6	5.0	245	1	A47539	homeotic protein g	185	6	5.0	360	2	D71888	lipid-a-disacchari
113	6	5.0	245	2	S78698	probable export pr	186	6	5.0	361	2	S68268	apurinic/aprimidi
114	6	5.0	245	2	G86869	probable export pr	187	6	5.0	364	2	A71443	probable inositol
115	6	5.0	245	2	G85812	flagellar biosynth	188	6	5.0	365	2	S56792	hypothetical prote
116	6	5.0	246	2	T12585	Dc3 promoter-bind	189	6	5.0	366	1	S70674	probable hydro-ly
117	6	5.0	247	2	T15579	hypothetical prote	190	6	5.0	366	2	T25178	hypothetical prote
118	6	5.0	248	2	B83764	transcription regu	191	6	5.0	367	2	S19172	cytochrome P450 2B
119	6	5.0	250	2	H82079	protein disulfide-	192	6	5.0	370	2	C83120	probable RND efflu
120	6	5.0	251	2	S75312	hypothetical prote	193	6	5.0	372	2	S69064	hypothetical prote
121	6	5.0	251	2	T24485	hypothetical prote	194	6	5.0	372	2	A41792	homeotic protein e
122	6	5.0	253	2	A5183	GS2 protein - huma	195	6	5.0	373	2	B96798	extensin [imported
123	6	5.0	258	2	S35276	probable export pr	196	6	5.0	375	2	B1842	carbamoyl-phosphat
124	6	5.0	261	2	H70933	hypothetical prote	197	6	5.0	375	2	E84674	carbamoyl-phosphat
125	6	5.0	261	2	F81376	probable integral	198	6	5.0	375	2	D75568	N-acetylamino acid r
126	6	5.0	267	2	T08283	hypothetical prote	199	6	5.0	377	2	B30341	G protein-coupled
127	6	5.0	268	1	JQ0961	myb-related protei	200	6	5.0	379	2	T11414	ubiquinol--cytochr
128	6	5.0	268	2	T46902	hypothetical prote	201	6	5.0	380	2	S39600	class I histocoma
129	6	5.0	271	2	G64025	hypothetical prote	202	6	5.0	385	1	S76874	probable hydro-ly
130	6	5.0	273	2	D71180	probable ribosomal	203	6	5.0	387	2	I50703	transcription fact
131	6	5.0	278	2	S18545	rab28 protein - ma	204	6	5.0	388	1	DEH0PT	pyruvate dehydroge
132	6	5.0	278	2	T23291	hypothetical prote	205	6	5.0	388	2	B70878	probable transfe
133	6	5.0	279	2	H83811	hypothetical prote	206	6	5.0	388	2	F69536	conserved hypotet
134	6	5.0	281	2	A38090	N-hydroxyarylamine	207	6	5.0	390	2	G82844	cysteine synthase
135	6	5.0	282	2	S39972	leucine-rich prote	208	6	5.0	391	2	H70041	probable transcrip
136	6	5.0	283	2	A69517	conserved hypotet	209	6	5.0	392	2	S72936	UDP-glucuronosyltr
137	6	5.0	284	2	S71227	extensin 1 - Arabi	210	6	5.0	392	2	C72783	hypothetical prote
138	6	5.0	286	2	F82881	hypothetical prote	211	6	5.0	393	2	S25331	probable methionyl
139	6	5.0	289	2	T16530	hypothetical prote	212	6	5.0	395	2	S38812	cyclin A - chicken
140	6	5.0	292	2	F72208	conserved hypotet	213	6	5.0	399	1	S38656	teta protein - Pse
141	6	5.0	293	2	F72409	conserved hypotet	214	6	5.0	399	1	YTECRL	tetracycline resis
142	6	5.0	293	2	T23806	hypothetical prote	215	6	5.0	399	2	J01479	tetracycline resis
143	6	5.0	294	2	A57478	serine O-acetyltra	216	6	5.0	399	2	S36719	FUN33 protein - ya
144	6	5.0	295	2	T20629	hypothetical prote	217	6	5.0	402	1	S25077	monensin polyketid
145	6	5.0	300	2	S54717	probable transcrip	218	6	5.0	406	2	T21271	hypothetical prote
146	6	5.0	300	2	T49748	hypothetical prote	219	6	5.0	409	2	T31662	hypothetical prote
147	6	5.0	302	2	F75619	hypothetical prote	220	6	5.0	411	2	B82682	succinylornithine
148	6	5.0	304	2	I50721	probable hemin ABC	221	6	5.0	412	2	T46681	probable glycosylt
149	6	5.0	309	2	T43752	synemin - chicken	222	6	5.0	414	2	A72765	hypothetical prote
150	6	5.0	312	2	S71207	site-specific DNA	223	6	5.0	415	2	T44601	probable glycosylt
151	6	5.0	316	2	H86665	serine O-acetyltra	224	6	5.0	415	2	E83544	hypothetical prote
152	6	5.0	320	2	F89747	ferrichrome ABC tr	225	6	5.0	416	2	T31486	hypothetical prote
153	6	5.0	322	2	T40718	two-component sens	226	6	5.0	418	2	A37344	acrosin (EC 3.4.21
154	6	5.0	322	2	T40718	probable transmem	227	6	5.0	418	2	T19800	hypothetical prote
155	6	5.0	328	1	HLHUCD	T-cell surface gly	228	6	5.0	420	2	A55283	acrosin (EC 3.4.21
156	6	5.0	328	1	S32369	gamma-SNAP protein	229	6	5.0	421	2	I49734	HNF-3/forx-head ho
157	6	5.0	329	2	T23924	hypothetical prote	230	6	5.0	422	2	T47065	hypothetical prote
158	6	5.0	332	2	T46239	hypothetical prote	231	6	5.0	430	2	C70176	probable ATP-depen
159	6	5.0	333	1	HLHUCB	T-cell surface gly	232	6	5.0	431	1	ZTEC3	citrate utilizatio
160	6	5.0	333	2	S76782	D-2-hydroxy-acid d	233	6	5.0	431	1	ZTEC6	probable membrane
161	6	5.0	334	2	B96657	probable replicati	234	6	5.0	431	2	T36570	hypothetical prote
162	6	5.0	335	1	A25968	exodeoxyribonuclea	235	6	5.0	432	2	T05236	citrate carrier pr
163	6	5.0	335	1	HLHUR3	DNA-directed RNA p	236	6	5.0	432	2	JQ0576	chaperonin 60 beta
164	6	5.0	336	2	I56235	T-cell surface gly	237	6	5.0	435	2	S56644	glucose-inhibited
165	6	5.0	337	2	I48682	rat CDI antigen pr	238	6	5.0	435	2	A72339	probable transposa
166	6	5.0	337	2	I57038	NEX-1 - mouse	239	6	5.0	439	2	H70582	hypothetical prote
167	6	5.0	342	2	S63654	gene Dlx-3 protein	240	6	5.0	442	1	Q0BYET	hypothetical prote
168	6	5.0	343	2	G86709	hypothetical COI i	241	6	5.0	446	2	F82609	aminopeptidase p x
169	6	5.0	344	2	JH0511	hypothetical prote	242	6	5.0	454	2	T42680	hypothetical prote
170	6	5.0	344	2	H83928	myo-inositol 2-deh	243	6	5.0	457	2	E96572	amidophosphoribosy
171	6	5.0	345	2	E85012	hypothetical prote	244	6	5.0	464	2	A28569	protein F12M16.8 [
172	6	5.0	345	2	B85881	hypothetical prote	245	6	5.0	470	2	D83938	alpha-methyl dopa-h
173	6	5.0	347	2	T09140	serine O-acetyltra	246	6	5.0	472	2	T22188	hypothetical prote
174	6	5.0	347	2	S76278	ABC-type transport	247	6	5.0				
175	6	5.0	349	1	G64096	D-galactose-bindin	248	6	5.0				

249	6	5.0	477	2	H86466	protein F23M19.7 [322	6	5.0	621	2	A83421	peptidyl-prolyl ci
250	6	5.0	479	1	A54040	adenosylhomocystei	323	6	5.0	633	2	T47524	hypothetical prote
251	6	5.0	481	2	S47091	cyclase-associated	324	6	5.0	635	2	C81861	hypothetical prote
252	6	5.0	481	2	T39357	hypothetical prote	325	6	5.0	640	2	T08758	hypothetical prote
253	6	5.0	484	2	S67820	GumD protein - xan	326	6	5.0	654	2	B84690	hypothetical prote
254	6	5.0	485	2	T04840	hypothetical prote	327	6	5.0	658	1	S73805	DNA ligase (NAD+)
255	6	5.0	491	1	O4RTPB	cytochrome P450 2B	328	6	5.0	663	2	T30621	hypothetical prote
256	6	5.0	491	1	O4RTPE	cytochrome P450 2B	329	6	5.0	667	2	S66017	formate dehydrogen
257	6	5.0	491	1	O4RBPC	cytochrome P450 2B	330	6	5.0	670	1	E70040	conserved dehydrog
258	6	5.0	491	2	JT0676	cytochrome P450 2B	331	6	5.0	671	2	D84648	probable disease r
259	6	5.0	491	2	S31277	cytochrome P450 2B	332	6	5.0	671	2	E82960	hypothetical prote
260	6	5.0	491	2	S31278	cytochrome P450 2B	333	6	5.0	684	2	T43452	hypothetical prote
261	6	5.0	491	2	S35666	cytochrome P450 2B	334	6	5.0	686	2	T06700	hypothetical prote
262	6	5.0	491	2	A27717	cytochrome P450 2B	335	6	5.0	690	2	E84724	hypothetical prote
263	6	5.0	491	2	A31047	testosterone 16alp	336	6	5.0	695	2	T07283	hypothetical prote
264	6	5.0	491	2	A32969	cytochrome P450 2B	337	6	5.0	698	2	D84547	hypothetical prote
265	6	5.0	491	2	T49625	testosterone 16a-h	338	6	5.0	701	2	A83677	hypothetical prote
266	6	5.0	491	2	T84735	testosterone 16a-h	339	6	5.0	704	2	S46000	probable membrane
267	6	5.0	492	2	S27160	cytochrome P450 2B	340	6	5.0	725	1	Z2BEA4	rapid lysis protei
268	6	5.0	494	2	S11305	cytochrome P450 2B	341	6	5.0	727	2	T26096	hypothetical prote
269	6	5.0	497	2	T32728	hypothetical prote	342	6	5.0	727	2	A54051	glycerol-3-phospha
270	6	5.0	499	2	B81914	probable periplasm	343	6	5.0	728	1	S59553	arginine decarboxy
271	6	5.0	500	2	B31047	testosterone 16alp	344	6	5.0	731	2	T44846	catalase (EC 1.11.
272	6	5.0	502	2	A82234	gonadoliberin III-	345	6	5.0	737	2	S47857	basic protein, cyt
273	6	5.0	507	2	T26809	hypothetical prote	346	6	5.0	738	2	A53542	brefeldin A-sensit
274	6	5.0	507	2	S23348	hypothetical prote	347	6	5.0	739	2	T15215	hypothetical prote
275	6	5.0	509	2	I45713	Dpp receptor TRV,	348	6	5.0	744	2	A70385	DNA gyrase A subun
276	6	5.0	509	2	G82809	amino acid transpo	349	6	5.0	751	2	F83080	hypothetical prote
277	6	5.0	510	2	S77380	lysine--trNA ligas	350	6	5.0	752	2	G82798	hypothetical prote
278	6	5.0	510	2	A32380	nuclear protein fk	351	6	5.0	760	2	H84427	hypothetical prote
279	6	5.0	511	2	E75561	probable phytoene	352	6	5.0	761	2	E85359	hypothetical prote
280	6	5.0	512	2	S06115	alpha-amylase (EC	353	6	5.0	779	1	S40382	box A-binding fact
281	6	5.0	512	2	S23355	alpha-amylase (EC	354	6	5.0	800	2	S13032	3',5'-cyclic-GMP p
282	6	5.0	513	2	T49365	hypothetical prote	355	6	5.0	802	2	H84740	hypothetical prote
283	6	5.0	513	2	C82366	conserved hypotet	356	6	5.0	802	1	A37142	outer membrane ush
284	6	5.0	516	2	S42093	cellulose 1,4-beta	357	6	5.0	803	2	A86655	hypothetical prote
285	6	5.0	519	2	A82634	2-isopropylmalate	358	6	5.0	804	2	D72257	DNA gyrase, subuni
286	6	5.0	526	2	T41944	hypothetical prote	359	6	5.0	809	2	G75605	hypothetical prote
287	6	5.0	527	1	T42934	thymidine kinase (360	6	5.0	810	2	S75931	hypothetical prote
288	6	5.0	527	2	S12158	hypothetical prote	361	6	5.0	810	2	D6818	hypothetical prote
289	6	5.0	529	2	B24059	t complex polypept	362	6	5.0	812	2	T07745	phosphatidylinosit
290	6	5.0	530	2	A81323	arginine--trNA lig	363	6	5.0	814	2	T07761	phosphatidylinosit
291	6	5.0	534	2	T29059	probable 2-isoprop	364	6	5.0	818	2	T01105	disease resistance
292	6	5.0	545	2	S31563	heat shock protein	365	6	5.0	820	2	H82302	Atp-dependent heli
293	6	5.0	545	2	H70180	heat shock protein	366	6	5.0	823	2	F64526	adenine/cytosine D
294	6	5.0	547	2	I40331	Cpn60 protein (Gro	367	6	5.0	824	2	F72408	leucine--trNA liga
295	6	5.0	547	2	B43606	heat shock protein	368	6	5.0	824	2	I52835	H-NUC - human
296	6	5.0	547	2	B83098	GroEL protein PA43	369	6	5.0	831	2	D96639	protein Tlf9.12 [i
297	6	5.0	549	2	C83677	L-lactate permease	370	6	5.0	831	2	S26675	DNA-directed DNA p
298	6	5.0	550	2	S61297	heat-shock protein	371	6	5.0	831	2	JX0359	DNA-directed DNA p
299	6	5.0	551	2	S30691	arylsulfatase (EC	372	6	5.0	832	2	A33530	DNA-directed DNA p
300	6	5.0	551	2	E86066	arylsulfatase (imp	373	6	5.0	835	2	T26086	hypothetical prote
301	6	5.0	552	2	S39765	chaperonin 60 - Co	374	6	5.0	849	2	H84546	hypothetical prote
302	6	5.0	553	2	S53080	hypothetical prote	375	6	5.0	853	2	A36617	3',5'-cyclic-GMP p
303	6	5.0	554	2	T36653	probable cation tr	376	6	5.0	854	2	A42828	3',5'-cyclic-GMP p
304	6	5.0	556	2	S13163	t-complex-type mol	377	6	5.0	856	2	S30762	3',5'-cyclic-GMP p
305	6	5.0	556	2	S10486	t-complex-type mol	378	6	5.0	864	2	T10970	DNA topoisomerase
306	6	5.0	556	2	JH0475	t complex polypept	379	6	5.0	864	2	D84740	hypothetical prote
307	6	5.0	556	2	JC1443	t complex polypept	380	6	5.0	887	2	S43196	uridyltransferas
308	6	5.0	556	2	JQ0866	t-complex protein	381	6	5.0	889	2	T09055	protocadherin 68 -
309	6	5.0	556	2	T39383	t-complex protein	382	6	5.0	890	2	G64740	uridyltransferas
310	6	5.0	559	2	A39793	t-complex-type mol	383	6	5.0	890	2	A85501	hypothetical prote
311	6	5.0	565	2	T32843	hypothetical prote	384	6	5.0	890	2	A30481	bacteriocin BCN5 -
312	6	5.0	568	2	B86400	hypothetical prote	385	6	5.0	895	2	T00800	disease resistance
313	6	5.0	570	2	T46911	hypothetical prote	386	6	5.0	895	2	E64431	UDPglucose 6-dehyd
314	6	5.0	572	1	S28762	gene Dbp73D protei	387	6	5.0	896	2	H86762	ABC transporter pe
315	6	5.0	576	2	A48765	G protein-coupled	388	6	5.0	907	2	E96636	hypothetical prote
316	6	5.0	594	2	T45842	calcium dependent	389	6	5.0	908	2	C70168	DNA polymerase I (
317	6	5.0	598	2	T42070	protein serine/thr	390	6	5.0	922	2	T37256	metalloproteinase
318	6	5.0	602	2	G81654	conserved hypotet	391	6	5.0	932	2	S47597	mutL protein homol
319	6	5.0	602	2	F71496	hypothetical prote	392	6	5.0	934	2	T02742	probable ligand-ga
320	6	5.0	605	2	T19818	hypothetical prote	393	6	5.0	942	2	T19553	hypothetical prote
321	6	5.0	611	2	F82442	probable peptide A	394	6	5.0	944	2	S01909	hairy wing suppres

395	6	5.0	958	2	T26258	hypothetical prote	468	5	4.1	36	2	B31872	retinoic acid-bind
396	6	5.0	977	2	I52657	seizure-related pr	469	5	4.1	36	2	JA0173	basic peptide - wi
397	6	5.0	984	2	T44496	cellulose 1,4-beta	470	5	4.1	39	2	C22102	phycoerythrin-545
398	6	5.0	989	2	T15576	hypothetical prote	471	5	4.1	40	2	C53288	major pollen aller
399	6	5.0	1004	2	S51133	hypothetical prote	472	5	4.1	42	4	S49124	nephritogenic prot
400	6	5.0	1007	2	T33285	transposase Tn4652	473	5	4.1	42	4	A39071	frame shifted G12_
401	6	5.0	1008	2	T05578	hypothetical prote	474	5	4.1	43	2	S18173	metallothionein -
402	6	5.0	1014	2	S75724	hypothetical prote	475	5	4.1	43	2	S18174	metallothionein -
403	6	5.0	1018	2	T15297	hypothetical prote	476	5	4.1	43	2	S33382	metallothionein -
404	6	5.0	1021	2	A28199	hypothetical prote	477	5	4.1	44	2	T07762	ribosomal protein
405	6	5.0	1021	2	A28199	hypothetical prote	478	5	4.1	44	2	T07762	ribosomal protein
406	6	5.0	1042	2	T16169	hypothetical prote	479	5	4.1	45	2	S28397	T-complex protein
407	6	5.0	1047	2	T23782	hypothetical prote	480	5	4.1	45	2	A84143	hypothetical prote
408	6	5.0	1055	2	T31111	ATPase 1 (EC 3.6.1	481	5	4.1	46	2	G70224	hypothetical prote
409	6	5.0	1063	1	S06206	grainy-head protei	482	5	4.1	48	1	R5VF32	ribosomal protein
410	6	5.0	1063	1	S06206	grainy-head protei	483	5	4.1	49	2	D82447	hypothetical prote
411	6	5.0	1082	2	T31112	ATPase 2 (EC 3.6.1	484	5	4.1	50	2	S32546	cytochrome c555 -
412	6	5.0	1160	2	T23713	hypothetical prote	485	5	4.1	50	2	H82588	hypothetical prote
413	6	5.0	1197	2	T28628	Y4CA protein - Rhl	486	5	4.1	50	2	A47694	nitrate reductase
414	6	5.0	1225	2	T32555	probable C2 domain	487	5	4.1	52	2	H82682	hypothetical prote
415	6	5.0	1226	2	E82328	5-methyltetrahydro	488	5	4.1	53	2	H82612	hypothetical prote
416	6	5.0	1230	2	S56850	SMC1 protein homol	489	5	4.1	54	2	H81933	hypothetical prote
417	6	5.0	1234	2	E83415	methionine synthas	490	5	4.1	55	1	R5NT32	ribosomal protein
418	6	5.0	1250	2	E81339	probable restricti	491	5	4.1	55	2	A24633	M protein - Strept
419	6	5.0	1273	1	TDFTLT	leukocyte common a	492	5	4.1	55	2	T09464	H+-transporting At
420	6	5.0	1276	1	DVMS2	multidrug resistan	493	5	4.1	55	2	S35675	protein kinase - r
421	6	5.0	1277	1	DVHY1C	multidrug resistan	494	5	4.1	56	2	A27579	T-cell receptor be
422	6	5.0	1278	2	S41646	p-glycoprotein - r	495	5	4.1	57	2	F81889	hypothetical prote
423	6	5.0	1281	2	I48123	p-glycoprotein - r	496	5	4.1	57	2	D81226	hypothetical prote
424	6	5.0	1286	2	T23714	p-glycoprotein iso	497	5	4.1	58	2	B25486	T-kininogen, LMW I
425	6	5.0	1295	2	T30528	hypothetical prote	498	5	4.1	58	2	T07400	TPS11 protein, pho
426	6	5.0	1307	2	T23106	reverse transcript	499	5	4.1	59	2	B69359	LSU ribosomal prot
427	6	5.0	1371	1	VCBEM7	hypothetical prote	500	5	4.1	60	2	S62188	hypothetical prote
428	6	5.0	1371	1	T42938	major capsid prote	501	5	4.1	61	2	S75172	hypothetical prote
429	6	5.0	1413	2	G84790	probable ABC trans	502	5	4.1	61	2	A83979	hypothetical prote
430	6	5.0	1421	2	T02501	hypothetical prote	503	5	4.1	63	2	C34620	metallothionein -
431	6	5.0	1445	2	T50508	hypothetical prote	504	5	4.1	63	2	S08191	metallothionein 2
432	6	5.0	1450	2	T45888	ABC transporter-li	505	5	4.1	63	2	S33381	metallothionein -
433	6	5.0	1510	2	T33100	hypothetical prote	506	5	4.1	63	2	A34620	metallothionein -
434	6	5.0	1519	2	S41525	hypothetical prote	507	5	4.1	63	2	A34958	metallothionein -
435	6	5.0	1533	2	T00344	major ring-forming	508	5	4.1	64	2	B69289	conserved hypothet
436	6	5.0	1547	2	T13847	hypothetical prote	509	5	4.1	64	2	B69384	conserved hypothet
437	6	5.0	1622	2	JE0378	sno (cytosine-5)-	510	5	4.1	64	2	E82738	hypothetical prote
438	6	5.0	1630	2	S64403	ESPI protein - yea	511	5	4.1	65	2	T06349	glucan endo-1,3-be
439	6	5.0	1711	2	T21432	hypothetical prote	512	5	4.1	65	2	S34538	hypothetical prote
440	6	5.0	1724	2	T13942	UNC-13-B protein -	513	5	4.1	68	1	G64421	hypothetical prote
441	6	5.0	1768	2	T13349	parallel sister ch	514	5	4.1	69	2	A05061	hypothetical prote
442	6	5.0	1784	2	C96615	hypothetical prote	515	5	4.1	69	2	F49410	t-complex polypept
443	6	5.0	1872	2	T30888	vitellogenin - Ath	516	5	4.1	69	2	T04350	auxin-induced prot
444	6	5.0	1963	1	MWKK	myosin heavy chain	517	5	4.1	69	2	PS0368	protein-tyrosine-p
445	6	5.0	2131	2	S01446	hypothetical prote	518	5	4.1	70	2	T07575	ribosomal protein
446	6	5.0	2274	2	T30258	adenomatous polyo	519	5	4.1	70	2	G42524	A-ORF-K protein -
447	6	5.0	2374	2	T21052	hypothetical prote	520	5	4.1	71	2	I49258	fibrosin - mouse (
448	6	5.0	2405	2	T08164	dynein alpha heavy	521	5	4.1	72	2	S32933	hypothetical prote
449	6	5.0	2489	2	S59782	probable membrane	522	5	4.1	72	2	C39370	hypothetical prote
450	6	5.0	2609	2	T40399	probable transport	523	5	4.1	73	2	T16615	rhombotin homolog
451	6	5.0	2670	2	T37919	GCN1 homolog - fis	524	5	4.1	73	2	T30612	hypothetical prote
452	6	5.0	2769	1	URBO	thyroglobulin prec	525	5	4.1	73	2	T31216	hypothetical prote
453	6	5.0	3161	2	T30342	protein HMWp1 - Ye	526	5	4.1	74	2	A71572	hypothetical prote
454	6	5.0	3163	2	T17440	probable polyketid	527	5	4.1	74	2	I51092	gonadotropin relea
455	6	5.0	3421	1	WZBEB6	367K tegument prot	528	5	4.1	74	2	F81671	conserved hypothet
456	6	5.0	3534	2	T42567	tegument protein 2	529	5	4.1	74	2	F83837	hypothetical prote
457	6	5.0	9376	2	T14593	syringomycin synth	530	5	4.1	75	2	S63585	ribosomal protein
458	6	5.0	9376	2	T14593	seed protein ws-5	531	5	4.1	77	2	T04345	auxin-induced prot
459	5	4.1	19	2	S19532	globin - polychaet	532	5	4.1	77	2	S45375	gene 43 protein -
460	5	4.1	21	2	S78575	protein kinase C i	533	5	4.1	77	2	S30988	very hypothetical
461	5	4.1	30	2	S55462	mer5 protein homol	534	5	4.1	77	2	T34983	hypothetical prote
462	5	4.1	30	2	C85851	hypothetical prote	535	5	4.1	77	2	T01280	gas-vesicle protei
463	5	4.1	30	2	S74112	proline-rich antib	536	5	4.1	78	2	S11923	conserved hypothet
464	5	4.1	30	4	S12902	diphtheria toxin f	537	5	4.1	78	2	G69033	tyrosine--tRNA lig
465	5	4.1	31	2	I52232	tau protein - huma	538	5	4.1	78	2	S75256	ig alpha chain - h
466	5	4.1	33	2	A03150	retinoic acid-bind	539	5	4.1	78	2	S24710	hypothetical prote
467	5	4.1	36	2	A29164	cartilage proteogl	540	5	4.1	78	2	F83869	

541 5 4.1 79 1 A58656 adipokinetic hormo
542 5 4.1 79 2 S53837 H-transferring Ar
543 5 4.1 79 2 T04352 auxin-induced prot
544 5 4.1 79 2 C71901 hypohetical prote
545 5 4.1 80 2 T17813 hypohetical prote
546 5 4.1 80 2 T28256 ORF MSV095 hypothe
547 5 4.1 81 2 B69958 hypohetical prote
548 5 4.1 81 2 T36197 probable acyl carr
549 5 4.1 81 2 E84002 hypohetical prote
550 5 4.1 82 2 I50966 MHC class II beta
551 5 4.1 82 2 I50973 MHC class II beta
552 5 4.1 82 2 T32723 ribosomal protein
553 5 4.1 82 2 B28945 ranatensin precurs
554 5 4.1 82 2 D69087 hydrogenase expres
555 5 4.1 82 2 E84301 hypohetical prote
556 5 4.1 82 2 T30135 hypohetical prote
557 5 4.1 82 2 I51180 gonadotropin-relea
558 5 4.1 82 2 I51355 gonadotropin relea
559 5 4.1 82 2 I51365 gonadotropin-relea
560 5 4.1 82 2 I51331 gonadotropin relea
561 5 4.1 82 2 T00185 hypohetical prote
562 5 4.1 83 2 S04884 seed protein (clon
563 5 4.1 83 2 T18122 hypohetical prote
564 5 4.1 84 2 T07939 embryonic abundant
565 5 4.1 84 2 E83004 glutaredoxin PA512
566 5 4.1 84 2 E82510 hypohetical prote
567 5 4.1 84 2 E64032 hypohetical prote
568 5 4.1 84 2 G64364 hypohetical prote
569 5 4.1 84 2 S57545 probable membrane
570 5 4.1 84 2 F72497 hypohetical prote
571 5 4.1 85 2 T31530 hypohetical prote
572 5 4.1 86 2 S78488 Ig kappa chain V r
573 5 4.1 86 2 G42523 A-ORF-B protein -
574 5 4.1 87 2 S69490 bombyxin B-10 - si
575 5 4.1 87 2 J00836 bombyxin B-10 - si
576 5 4.1 87 2 A82756 hypohetical prote
577 5 4.1 88 2 T31230 hypohetical prote
578 5 4.1 89 2 B86833 hypohetical prote
579 5 4.1 89 2 J02361 wheat aluminum ind
580 5 4.1 90 2 J07395 salmon-type gonado
581 5 4.1 90 2 A23735 gonadoliberin prec
582 5 4.1 90 2 I51095 gonadoliberin prec
583 5 4.1 91 2 T11359 NADH dehydrogenase
584 5 4.1 91 2 S16249 embryonic abundant
585 5 4.1 91 2 T09285 embryonic abundant
586 5 4.1 91 2 T09293 hypohetical prote
587 5 4.1 91 2 E86512 hypohetical prote
588 5 4.1 91 2 C64539 hypohetical prote
589 5 4.1 91 2 A71968 Mutr/nudix family
590 5 4.1 91 2 D75561 hypohetical prote
591 5 4.1 91 2 S54546 hypohetical prote
592 5 4.1 91 2 D72109 gonadoliberin I pr
593 5 4.1 92 2 I50644 gonadoliberin I pr
594 5 4.1 92 2 S23527 embryonic abundant
595 5 4.1 92 2 JQ2273 embryonic abundant
596 5 4.1 92 2 S34802 embryogenic abunda
597 5 4.1 92 2 S71372 embryonic abundant
598 5 4.1 92 2 B82066 phosphocarrier pro
599 5 4.1 92 2 T76007 hypohetical prote
600 5 4.1 92 2 D81731 conserved hypohet
601 5 4.1 93 2 S43333 embryonic abundant
602 5 4.1 93 2 S46303 gB19.lb protein -
603 5 4.1 93 2 S43332 EmH5 protein - whe
604 5 4.1 93 2 S23749 embryonic abundant
605 5 4.1 93 2 A27519 Em protein - whea
606 5 4.1 93 2 G64641 conserved hypohet
607 5 4.1 93 2 H71872 glu-tRNA amidotran
608 5 4.1 93 2 E64336 conserved hypohet
609 5 4.1 93 2 A85839 hypohetical prote
610 5 4.1 93 2 S72339 hypohetical prote
611 5 4.1 94 1 VUMTEM embryonic abundant
612 5 4.1 94 2 S30186 NADH dehydrogenase
613 5 4.1 95 2 A61629 retinoic acid-bind

614 5 4.1 95 2 S22483 embryonic abundant
615 5 4.1 95 2 E86447 protein F5D14.5 [1
616 5 4.1 95 2 B71571 hypohetical prote
617 5 4.1 96 2 S73002 hypohetical prote
618 5 4.1 97 1 D69961 lipoprotein homolo
619 5 4.1 97 2 S16028 Ig heavy chain V r
620 5 4.1 97 2 T17861 hypohetical prote
621 5 4.1 98 2 T14136 NADH dehydrogenase
622 5 4.1 98 2 I57601 tubulin alpha chai
623 5 4.1 98 2 G64693 hypohetical prote
624 5 4.1 98 2 D71807 hypohetical prote
625 5 4.1 98 2 E82394 hypohetical prote
626 5 4.1 98 2 T36896 hypohetical prote
627 5 4.1 99 2 T10839 embryonic abundant
628 5 4.1 99 2 G64469 hypohetical prote
629 5 4.1 99 2 T02894 hypohetical prote
630 5 4.1 100 1 A36138 urease (EC 3.5.1.5
631 5 4.1 100 1 B43719 urease (EC 3.5.1.5
632 5 4.1 100 1 S08478 urease (EC 3.5.1.5
633 5 4.1 100 2 B47090 urease (EC 3.5.1.5
634 5 4.1 100 2 D85603 probable urease st
635 5 4.1 100 2 E85654 probable urease st
636 5 4.1 100 2 S13796 retinoic acid-bind
637 5 4.1 100 2 D96528 protein F27J15.8 [1
638 5 4.1 100 2 C84642 probable steroid b
639 5 4.1 101 2 S46383 ribosomal protein
640 5 4.1 101 2 C72741 hypohetical prote
641 5 4.1 101 2 S69785 prgJ protein - Sal
642 5 4.1 101 2 B72638 hypohetical prote
643 5 4.1 102 2 B49056 T-cell receptor al
644 5 4.1 102 2 S19225 embryonic abundant
645 5 4.1 102 2 H81322 probable efflux pr
646 5 4.1 102 2 T33558 hypohetical prote
647 5 4.1 102 2 E72619 hypohetical prote
648 5 4.1 103 2 S40134 T-cell receptor V-
649 5 4.1 103 2 C75513 conserved hypohet
650 5 4.1 103 2 C86411 protein FLK3.22 [1
651 5 4.1 104 2 T36424 probable ABC-type
652 5 4.1 105 2 T07087 embryonic abundant
653 5 4.1 105 2 S11410 hypohetical prote
654 5 4.1 105 2 H72736 hypohetical prote
655 5 4.1 105 2 B75035 hypohetical prote
656 5 4.1 105 4 S59325 hypohetical prote
657 5 4.1 106 2 F70081 hypohetical prote
658 5 4.1 106 2 S32964 hypohetical prote
659 5 4.1 106 2 B71659 hypohetical prote
660 5 4.1 106 2 E82605 conjugal transfer
661 5 4.1 106 2 H64345 hypohetical prote
662 5 4.1 106 2 B61600 segmentation prote
663 5 4.1 106 2 E84056 chloroedoxin H1 BH3
664 5 4.1 107 1 YVBPL lysis protein S -
665 5 4.1 107 2 F71604 ribosomal protein
666 5 4.1 107 2 S64117 hypohetical prote
667 5 4.1 107 2 S18529 hypohetical prote
668 5 4.1 107 2 D70598 hypohetical prote
669 5 4.1 107 2 H82558 hypohetical prote
670 5 4.1 108 1 JLB06 coupling factor 6
671 5 4.1 108 1 YVBPS2 hemagglutinin prec
672 5 4.1 108 1 YVBPS2 lysis protein S -
673 5 4.1 108 2 S24251 Ig heavy chain V r
674 5 4.1 108 2 J70563 coupling factor 6
675 5 4.1 108 2 C64463 hypohetical prote
676 5 4.1 108 2 G83073 hypohetical prote
677 5 4.1 108 2 A28667 hypohetical prote
678 5 4.1 108 2 G70694 hypohetical prote
679 5 4.1 109 2 E81231 50S ribosomal prot
680 5 4.1 109 2 T01654 ribosomal protein
681 5 4.1 109 2 B72213 conserved hypohet
682 5 4.1 109 2 S73589 hypohetical prote
683 5 4.1 109 2 B54743 transcription fact
684 5 4.1 110 1 R5BYAL acidic ribosomal p
685 5 4.1 110 2 A72728 hypohetical prote
686 5 4.1 110 2 T33508 hypohetical prote

687	5	4.1	111	2	S75752	hypothetical prote	101	4.1	124	2	D84319	30S ribosomal prot
688	5	4.1	111	2	JH0183	Sc4 protein - brac	760	4.1	124	2	F81942	probable regulator
689	5	4.1	111	2	T17582	hypothetical prote	761	4.1	124	2	A81163	conserved hypothet
690	5	4.1	111	2	A25573	minicircle a prote	762	4.1	124	2	A83707	hypothetical prote
691	5	4.1	111	2	T43426	glucosamine-phosph	763	4.1	125	2	A29879	mesotocin / neurop
692	5	4.1	112	1	SPRFA	substance P alpha	764	4.1	125	2	I52650	microtubule-associ
693	5	4.1	112	2	A27889	Ig heavy chain v r	765	4.1	125	2	D82380	chemotaxis protein
694	5	4.1	112	2	T10827	embryonic abundant	766	4.1	125	2	S21329	14K inner membrane
695	5	4.1	112	2	S46188	embryonic abundant	767	4.1	125	2	D70732	hypothetical prote
696	5	4.1	112	2	E70433	flagellar switch p	768	4.1	125	2	C64777	probable membrane
697	5	4.1	112	2	C54743	transcription fact	769	4.1	125	2	E85544	probable gene 58 p
698	5	4.1	112	2	B35308	CAMP-regulated pho	770	4.1	125	2	B83521	hypothetical prote
699	5	4.1	113	2	S13494	major oleosin chal	771	4.1	125	2	A35003	galactose-binding
700	5	4.1	113	2	S59116	programmed cell de	772	4.1	125	2	C83704	hypothetical prote
701	5	4.1	113	2	T17503	hypothetical prote	773	4.1	126	2	S29303	hypothetical prote
702	5	4.1	114	2	T09627	positive transcrip	774	4.1	126	2	T48831	hypothetical prote
703	5	4.1	114	2	D83373	conserved hypothet	775	4.1	126	2	F72729	hypothetical prote
704	5	4.1	114	2	S02049	hypothetical prote	776	4.1	126	2	D72570	hypothetical prote
705	5	4.1	114	2	T13629	hypothetical prote	777	4.1	126	2	F83536	hypothetical prote
706	5	4.1	114	2	T13324	hypothetical prote	778	4.1	126	2	E84225	probable ring-clea
707	5	4.1	114	2	H69894	delta-endotoxin ho	779	4.1	127	2	S16685	hypothetical prote
708	5	4.1	115	1	A33323	motilin precursor	780	4.1	128	2	S76759	Ig heavy chain v r
709	5	4.1	115	1	S37176	ribosomal protein	781	4.1	128	2	T08625	hypothetical prote
710	5	4.1	115	2	JC6511	motilin precursor	782	4.1	128	2	S12900	hypothetical prote
711	5	4.1	115	2	PH1557	Ig heavy chain v r	783	4.1	128	2	SPHUB	phycocerythrin alph
712	5	4.1	115	2	D70123	ribosomal protein	784	4.1	129	1	S69862	neurokinin 1 precu
713	5	4.1	115	2	S73268	photosystem II pro	785	4.1	129	2	S63422	hypothetical prote
714	5	4.1	115	2	F71532	hypothetical prote	786	4.1	129	2	S55044	probable membrane
715	5	4.1	115	2	T44558	hypothetical prote	787	4.1	129	2	C86771	NK-lysin protein -
716	5	4.1	115	2	A28336	hypothetical prote	788	4.1	129	2	G82095	hypothetical prote
717	5	4.1	115	2	A37258	hypothetical prote	789	4.1	129	2	SPRTB	transcription regu
718	5	4.1	115	2	B83058	hypothetical prote	790	4.1	130	1	SPBOB	substance P beta p
719	5	4.1	116	1	B64054	ribosomal protein	791	4.1	130	1	S47038	neurokinin 1 precu
720	5	4.1	116	2	T04060	conserved hypothet	792	4.1	130	2	I52526	tachykinin 1 precu
721	5	4.1	116	2	T14876	hypothetical prote	793	4.1	130	2	S37715	hypothetical prote
722	5	4.1	116	2	T33195	hypothetical prote	794	4.1	131	1	E69304	conserved hypothet
723	5	4.1	116	2	E72622	hypothetical prote	795	4.1	131	2	F82331	conserved hypothet
724	5	4.1	117	2	A28846	Ig heavy chain pre	796	4.1	131	2	S09893	hypothetical prote
725	5	4.1	118	2	T43791	non-specific lipid	797	4.1	131	2	C83546	hypothetical prote
726	5	4.1	118	2	I50813	MHC class I protei	798	4.1	131	2	A64649	hypothetical prote
727	5	4.1	118	2	I50814	MHC class I protei	799	4.1	131	2	T11570	hypothetical prote
728	5	4.1	118	2	S51207	cruxhalorhodopsin-	800	4.1	131	2	B60725	hypothetical prote
729	5	4.1	118	2	S45096	13K transport prot	801	4.1	131	2	C72636	hypothetical prote
730	5	4.1	118	2	S45099	13K transport prot	802	4.1	131	2	T30643	hypothetical prote
731	5	4.1	118	2	F58932	probable membrane	803	4.1	132	2	S15966	hypothetical prote
732	5	4.1	118	2	S64344	hypothetical prote	804	4.1	132	2	D82278	hypothetical prote
733	5	4.1	118	2	A32245	hypothetical prote	805	4.1	132	2	G84274	hypothetical prote
734	5	4.1	118	2	B81242	hypothetical prote	806	4.1	132	2	T08676	hypothetical prote
735	5	4.1	118	2	T27456	hypothetical prote	807	4.1	132	2	S36751	embryonic abundant
736	5	4.1	118	2	H72644	probable arabinoga	808	4.1	133	2	F70470	conserved hypothet
737	5	4.1	119	2	A65014	yfec protein - Esc	809	4.1	133	2	T26268	hypothetical prote
738	5	4.1	119	2	E85882	hypothetical prote	810	4.1	133	2	T39730	40S ribosomal prot
739	5	4.1	119	2	D75111	hypothetical prote	811	4.1	134	2	B69353	conserved hypothet
740	5	4.1	119	2	E72714	hypothetical prote	812	4.1	134	2	S75224	hypothetical prote
741	5	4.1	120	1	ZBBPG4	probable ribosomal	813	4.1	134	2	C75352	conserved hypothet
742	5	4.1	120	2	S27251	gene B protein - p	814	4.1	134	2	T20516	hypothetical prote
743	5	4.1	120	2	B72770	NADH dehydrogenase	815	4.1	134	2	D82589	hypothetical prote
744	5	4.1	120	2	T18015	hypothetical prote	816	4.1	135	2	F84678	hypothetical prote
745	5	4.1	120	2	E81095	hypothetical prote	817	4.1	135	2	D81337	probable ATP /GTP-
746	5	4.1	120	2	A84286	hypothetical prote	818	4.1	135	2	S72964	hypothetical prote
747	5	4.1	121	2	H27888	membrane anchor li	819	4.1	135	2	A32317	sex-regulated prot
748	5	4.1	121	2	D78888	Ig heavy chain v r	820	4.1	135	2	PH1559	Ig heavy chain v r
749	5	4.1	121	2	F84868	Ig heavy chain v r	821	4.1	136	2	D70361	transcription regu
750	5	4.1	121	2	F70208	hypothetical prote	822	4.1	136	2	T03208	hypothetical prote
751	5	4.1	121	2	B96647	conserved hypothet	823	4.1	136	2	T36547	hypothetical prote
752	5	4.1	122	2	S56024	hypothetical prote	824	4.1	136	2	T46432	hypothetical prote
753	5	4.1	122	2	C82926	hypothetical prote	825	4.1	136	2	RJH01	retinoic acid-bind
754	5	4.1	123	2	G27888	hypothetical prote	826	4.1	137	1	PH1562	Ig heavy chain v r
755	5	4.1	123	2	A39266	Ig heavy chain v r	827	4.1	137	2	A35825	retinoic acid-bind
756	5	4.1	123	2	S64246	heat shock protein	828	4.1	137	2	T04930	Ig heavy chain v r
757	5	4.1	123	2	G84592	hypothetical prote	829	4.1	137	2	B55220	glycine-rich cell
758	5	4.1	123	2	D72579	hypothetical prote	830	4.1	137	2	T02013	hypothetical prote
759	5	4.1	124	2	I27888	Ig heavy chain v r	831	4.1	137	2		
						832	4.1	137	2			

833	5	4.1	138	1	SWOD	diuretic hormone p	906	5	4.1	149	1	G70400	conserved hypothet
834	5	4.1	138	2	PH1564	Ig heavy chain v r	907	5	4.1	149	2	T09674	ribosomal protein
835	5	4.1	138	2	PH1565	Ig heavy chain v r	908	5	4.1	149	2	D83256	heat-shock protein
836	5	4.1	138	2	T43365	ribosomal protein	909	5	4.1	149	2	F72677	hypothetical prote
837	5	4.1	138	2	S24100	envelope protein -	910	5	4.1	150	2	S72852	hypothetical prote
838	5	4.1	138	2	D71172	hypothetical prote	911	5	4.1	150	2	C86754	prophage pi2 prote
839	5	4.1	138	2	T39043	hypothetical prote	912	5	4.1	150	2	S73725	probable transmem
840	5	4.1	138	2	T34049	hypothetical prote	913	5	4.1	150	2	C71297	hypothetical prote
841	5	4.1	138	2	T04516	hypothetical prote	914	5	4.1	151	1	E65001	hypothetical prote
842	5	4.1	139	2	JX0238	UDPglucose 4-epime	915	5	4.1	151	2	T16284	hypothetical prote
843	5	4.1	139	2	PH1558	Ig heavy chain v r	916	5	4.1	151	2	A96493	hypothetical prote
844	5	4.1	139	2	S43769	cold-regulated pro	917	5	4.1	151	2	A72409	conserved hypothet
845	5	4.1	139	2	S60916	probable membrane	918	5	4.1	152	2	I77327	NADH dehydrogenase
846	5	4.1	139	2	T03372	high mobility grou	919	5	4.1	152	2	S34819	embryonic abundant
847	5	4.1	140	1	IIMSG1	interleukin-4 prec	920	5	4.1	152	2	S19388	probable membrane
848	5	4.1	140	2	H71903	hypothetical prote	921	5	4.1	152	2	S64605	hypothetical prote
849	5	4.1	140	2	H82651	hypothetical prote	922	5	4.1	152	2	S64605	H+-transporting AT
850	5	4.1	140	2	G69986	hypothetical prote	923	5	4.1	153	2	S36752	embryonic abundant
851	5	4.1	141	2	S1685	Ig heavy chain v r	924	5	4.1	153	2	S73686	adhesin F1 homolog
852	5	4.1	141	2	I39059	hypothetical prote	925	5	4.1	153	2	T09832	water-stress-induc
853	5	4.1	141	2	C72606	hypothetical prote	926	5	4.1	153	2	S74290	DOM34 protein homo
854	5	4.1	141	2	C71906	hypothetical prote	927	5	4.1	154	2	S20511	superoxide dismuta
855	5	4.1	142	1	S01714	hemoglobin zeta ch	928	5	4.1	154	2	T00556	60S ribosomal prot
856	5	4.1	142	2	B70830	hypothetical prote	929	5	4.1	154	2	T47667	ribosomal L23a-lik
857	5	4.1	142	2	T44478	hypothetical prote	930	5	4.1	154	2	S49250	glycine cleavage s
858	5	4.1	142	2	T45922	probable C2H2-type	931	5	4.1	154	2	E82015	probable DNA trans
859	5	4.1	143	1	S04230	H+-transporting AT	932	5	4.1	154	2	C81819	hypothetical prote
860	5	4.1	143	1	S18241	alpha-amylase inh	933	5	4.1	154	2	T21023	RNA-binding protei
861	5	4.1	143	2	S34069	H+-transporting AT	934	5	4.1	154	2	JC4588	probable ribosomal
862	5	4.1	143	2	S49229	H-protein - Flaver	935	5	4.1	155	2	G72557	conserved hypothet
863	5	4.1	143	2	E59065	molybdopterin bios	936	5	4.1	155	2	D83098	hypothetical prote
864	5	4.1	143	2	H71970	hypothetical prote	937	5	4.1	155	2	T24828	glycine decarboxyl
865	5	4.1	143	2	D81751	conserved hypothet	938	5	4.1	156	2	H84764	hypothetical prote
866	5	4.1	143	2	D83148	hypothetical prote	939	5	4.1	156	2	D72473	hypothetical prote
867	5	4.1	143	2	JC5246	allograft inflamma	940	5	4.1	156	2	E83227	probable C2H2-type
868	5	4.1	143	2	T02951	hypothetical prote	941	5	4.1	156	2	C84688	hypothetical prote
869	5	4.1	144	1	YMSMCM	macromycin precu	942	5	4.1	156	2	E84861	hypothetical prote
870	5	4.1	144	1	A28123	transcription fact	943	5	4.1	156	2	S22446	T-cell translocati
871	5	4.1	144	2	PH1563	Ig heavy chain v r	944	5	4.1	156	2	A32795	hypothetical prote
872	5	4.1	144	2	I46642	rearranged T-cell	945	5	4.1	157	2	JC5551	hypothetical prote
873	5	4.1	144	2	F75470	hypothetical prote	946	5	4.1	157	2	S75191	hypothetical prote
874	5	4.1	144	2	H96511	AP2 domain contain	947	5	4.1	157	2	F71906	similar to S-locus
875	5	4.1	144	2	T14796	hypothetical prote	948	5	4.1	157	2	H84638	hypothetical prote
876	5	4.1	145	2	D81366	probable ribose 5-	949	5	4.1	157	2	H83807	hypothetical prote
877	5	4.1	145	2	S75219	hypothetical prote	950	5	4.1	158	2	S63140	ribosomal protein
878	5	4.1	145	2	T33139	hypothetical prote	951	5	4.1	158	2	F64607	hypothetical prote
879	5	4.1	145	2	A72804	gp34.1 protein - M	952	5	4.1	158	2	B84588	probable AP2 domai
880	5	4.1	145	2	C72668	hypothetical prote	953	5	4.1	158	2	H71229	hypothetical prote
881	5	4.1	145	2	H82110	hypothetical prote	954	5	4.1	159	2	G72249	ribosomal protein
882	5	4.1	145	2	F81338	probable periplasm	955	5	4.1	159	2	A72462	hypothetical prote
883	5	4.1	145	2	F83247	hypothetical prote	956	5	4.1	159	2	H81657	conserved hypothet
884	5	4.1	145	2	D70938	hypothetical prote	957	5	4.1	159	2	T00930	hypothetical prote
885	5	4.1	145	2	H82567	outer membrane pro	958	5	4.1	159	2	D82649	hypothetical prote
886	5	4.1	146	2	A44588	globin - waved whe	959	5	4.1	159	2	F84091	hypothetical prote
887	5	4.1	146	2	A47167	mucin-like endothe	960	5	4.1	159	2	A83295	hypothetical prote
888	5	4.1	146	2	JC4902	ionized calcium bi	961	5	4.1	159	2	S46494	galactoside 2-alph
889	5	4.1	146	2	T38048	very hypothetical	962	5	4.1	160	1	F70351	NADH dehydrogenase
890	5	4.1	146	2	S45128	hypothetical prote	963	5	4.1	160	2	S45632	H+-transporting AT
891	5	4.1	146	2	C72703	hypothetical prote	964	5	4.1	160	2	S47249	gene 1-Sc3 protein
892	5	4.1	147	2	PH1561	Ig heavy chain v r	965	5	4.1	160	2	S30054	major allergen Cor
893	5	4.1	147	2	G85749	conserved hypothet	966	5	4.1	160	2	S30055	major allergen Cor
894	5	4.1	147	2	G48552	ORF-US441 - Infect	967	5	4.1	160	2	S30056	major allergen Cor
895	5	4.1	147	2	JC7237	receptor-activity-	968	5	4.1	160	2	S30053	major allergen Cor
896	5	4.1	147	2	JC7263	receptor activity	969	5	4.1	160	2	T19458	hypothetical prote
897	5	4.1	147	2	I55617	allograft inflamma	970	5	4.1	160	2	F75450	hypothetical prote
898	5	4.1	147	2	H82313	hypothetical prote	971	5	4.1	160	2	C84422	hypothetical prote
899	5	4.1	147	2	T30606	hypothetical prote	972	5	4.1	161	1	USURAL	tubulin alpha chai
900	5	4.1	148	2	G75066	hypothetical prote	973	5	4.1	161	2	S71453	glycine-rich RNA-b
901	5	4.1	148	2	JC5281	sporozoite 60K pro	974	5	4.1	161	2	E71866	hypothetical prote
902	5	4.1	148	2	E81016	ComEA-related prot	975	5	4.1	162	2	E69155	hypothetical prote
903	5	4.1	148	2	C81214	ComEA-related prot	976	5	4.1	162	2	H69896	hypothetical prote
904	5	4.1	148	2	A84636	similar to avrRpt2	977	5	4.1	162	2	D96581	hypothetical prote
905	5	4.1	148	2	H83054	suppressor protein	978	5	4.1	162	2	C75497	hypothetical prote

979 5 4.1 163 2 C71977
980 5 4.1 163 2 S55278
981 5 4.1 163 2 G72639
982 5 4.1 163 2 A31768
983 5 4.1 163 2 E72473
984 5 4.1 164 1 NWU03
985 5 4.1 164 2 A40104
986 5 4.1 164 2 T47547
987 5 4.1 164 2 T26952
988 5 4.1 164 2 S27529
989 5 4.1 165 1 G55079
990 5 4.1 165 2 A36237
991 5 4.1 165 2 G84767
992 5 4.1 165 2 S50195
993 5 4.1 165 2 S35195
994 5 4.1 165 2 G85951
995 5 4.1 165 2 A39617
996 5 4.1 165 2 F72545
997 5 4.1 165 2 T01421
998 5 4.1 166 2 A86450
999 5 4.1 166 2 JC4664
1000 5 4.1 166 2 I46424

ALIGNMENTS

RESULT 1
A43779
neurokinin B precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 16-Jul-1999
C:Accession: A43779
R:Bonner, T.I.; Aflolter, H.U.; Young, A.C.; Young III, W.S.
Brain Res. Mol. Brain Res. 2, 243-249, 1987
A:Title: A cDNA encoding the precursor of the rat neuropeptide, neurokinin B.
A:Reference number: A43779
A:Accession: A43779
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <BON>
A:Cross-references: GB:M16410; GB:M35607; NID:g205724; PIDN:AAA41711.1; PID:g205725
C:Superfamily: neurokinin B precursor
C:Keywords: neuropeptide

Query Match 8.3%; Score 10; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDHDFVVG 88
| | | | | | | | | |
Db 80 KRDHDFVVG 89

RESULT 2
I65342
tachykinin B precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C:Accession: I65342
R:Kako, K.; Muneke, E.; Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 14, 253-259, 1993
A:Title: Cloning and sequence analysis of mouse cDNAs encoding preprotachykinin A and B.
A:Reference number: I52526
A:Accession: I65342
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-116 <RES>
A:Cross-references: GB:D14423; NID:g407346; PIDN:BAA03316.1; PID:g407347
A:Gene: PPT-B
C:Superfamily: neurokinin B precursor

Query Match 8.3%; Score 10; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDHDFVVG 88
| | | | | | | | | |
Db 80 KRDHDFVVG 89

RESULT 3
A25905
tachykinin B precursor - bovine
N:Alternate names: neuromedin K
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C:Accession: A25905
R:Kotani, H.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 83, 7074-7078, 1986
A:Title: Structure and gene organization of bovine neuromedin K precursor.
A:Reference number: A25905; MUID:86313713
A:Accession: A25905
A:Molecule type: DNA
A:Residues: 1-126 <KOT>
A:Cross-references: GB:M14351; NID:gl63587; PIDN:AAA30723.1; PID:gl63590
C:Superfamily: neurokinin B precursor
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-126/Product: protachykinin B #status predicted <MAT>

Query Match 8.3%; Score 10; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDHDFVVG 88
| | | | | | | | | |
Db 84 KRDHDFVVG 93

RESULT 4
SPFGNK
neuromedin K - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 23-Aug-1996
C:Accession: A01560
R:Kangawa, K.; Minamino, N.; Fukuda, A.; Matsuo, H.
Biochem. Biophys. Res. Commun. 114, 533-540, 1983
A:Title: Neuromedin K: a novel mammalian tachykinin identified in porcine spinal cord
A:Reference number: A01560; MUID:83282812
A:Accession: A01560
A:Molecule type: protein
A:Residues: 1-10 <KAN>
A>Note: the structure of the peptide was confirmed by synthesis
C:Comment: The biological source of this peptide is spinal cord. It stimulates smooth
C:Superfamily: neurokinin B precursor
C:Keywords: amidated carboxyl end; hormone; spinal cord
F:10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 DMHDFVVG 88
| | | | | | | |
Db 1 DMHDFVVG 8

RESULT 5
E75338
DNA gyrase, subunit A - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
A:Accession: E75338
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: E75338
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-812 <WHI>
A:Cross-references: GB:AE002030; GB:AE000513; NID:96459692; PIDN:AAF11467.1; PID:9645969
C:Experimental source: strain R1
C:Genetics:
A:Gene: DR1913
A:Map position: 1
C:Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase C

Query Match 6.6%; Score 8; DB 2; Length 812;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 57 LEGLLKAL 64
DB 377 LEGLLKAL 384
|||||

RESULT 6
S75133
hypothetical protein slr2101 - Synchocystis sp. (strain PCC 6803)
C:Species: Synchocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis
S.
A:Reference number: S74322; MUID:97061201
A:Accession: S75133
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-143 <KAN>
A:Cross-references: EMBL:D90910; GB:AB001339; NID:g1652956; PIDN:BAAL7995.1; PID:g165307
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 5.8%; Score 7; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 108 VPSFGIL 114
DB 75 VPSFGIL 81
|||||

RESULT 7
H70733
hypothetical protein Rv2300c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: H70733
R:Colle, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987
A:Accession: H70733

A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-310 <COL>
A:Cross-references: GB:277163; GB:AL123456; NID:g3261610; PIDN:CAB00971.1; PID:e25516
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV2300c

Query Match 5.8%; Score 7; DB 2; Length 310;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 DPDLXOL 46
DB 299 DPDLXOL 305
|||||

RESULT 8
T50468
probable maturase [imported] - Neurospora crassa mitochondrion
C:Species: mitochondrion Neurospora crassa
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C:Accession: T50468
R:Moreill, G.; Macino, G.
J. Mol. Biol. 178, 491-507, 1984
A>Title: Two intervening sequences in the ATPase subunit 6 gene of Neurospora crassa:
A:Reference number: 225077; MUID:85033713
A:Accession: T50468
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-366 <MOR>
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SGC3
C:Keywords: mitochondrion

Query Match 5.8%; Score 7; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 56 SLEGLLK 62
DB 178 SLEGLLK 184
|||||

RESULT 9
B82846
succinyl-diaminopimelate desuccinylase XF0116 [imported] - Xylella fastidiosa (strain
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C:Accession: B82846
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: B82846
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <SIM>
A:Cross-references: GB:AE003865; GB:AE003849; NID:g9104892; PIDN:AAF82929.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carrier
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A.; Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0116
C:Superfamily: succinyl-diaminopimelate desuccinylase

Query Match 5.8%; Score 7; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 PDLYQLL 47

Db 363 PDLYQLL 369

RESULT 10

E75439 conserved hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C:Accession: E75439

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896

A:Accession: E75439

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-394 <WHI>

A:Cross-references: GB:AE001958; GB:AE000513; NID:g6458805; PIDN:AAF10648.1; PID:g645880

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR1075

A:Map position: 1

C:Superfamily: hypothetical protein slr0882

Query Match 5.8%; Score 7; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLFTAIL 11

Db 34 LLFTAIL 40

RESULT 11

C81351

probable UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanine 1

C:Species: Campylobacter jejuni

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Jun-2000

C:Accession: C81351

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A:Reference number: A81250; MUID:20150912

A:Accession: C81351

A:Molecule type: DNA

A:Residues: 1-475 <PAR>

A:Cross-references: GB:AL1139076; GB:AL111168; NID:g6968128; PIDN:CAB73060.1; PID:g696824

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: murF; Cj0795c

C:Keywords: ligase

Query Match 5.8%; Score 7; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 HSSLEGL 60

Db 295 HSSLEGL 301

RESULT 12

E96664

hypothetical protein T12P18.4 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: E96664

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Hughes, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Chung, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: E96664

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-493 <STO>

A:Cross-references: GB:AE005173; NID:g6358782; PIDN:AAF07363.1; GSPDB:GN00141

C:Genetics:

A:Gene: T12P18.4

A:Map position: 1

C:Superfamily: rubredoxin--NAD+ reductase rubB

Query Match 5.8%; Score 7; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 QLLQRLF 51

Db 250 QLLQRLF 256

RESULT 13

C83122

probable aldehyde dehydrogenase PA4189 [imported] - Pseudomonas aeruginosa (strain PA

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: C83122

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337

A:Accession: C83122

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-496 <STO>

A:Cross-references: GB:AE004835; GB:AE004091; NID:g9950394; PIDN:AAG07576.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA4189

C:Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology

Query Match 5.8%; Score 7; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 VVPGGGR 36
|||||||
Db 220 VVPGGGR 226

RESULT 14
D83775
hypothetical protein BH1004 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C:Accession: D83775
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20263314
A:Accession: D83775
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-534 <STO>
A:Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04723.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1004

Query Match 5.8%; Score 7; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MLLFTAI 10
|||||||
Db 87 MLLFTAI 93

RESULT 15
A54372
G protein-coupled receptor kinase (EC 2.7.1.1-) 5 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A54372
R:Premont, R.T.; Koch, W.J.; Inglesse, J.; Lefkowitz, R.J.
J. Biol. Chem. 269, 6832-6841, 1994
A:Title: Identification, purification, and characterization of GRK5, a member of the fam
A:Reference number: A54372; MUID:94165084
A:Accession: A54372
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-590 <PRE>
A:Cross-references: GB:U01206; NID:g437105; PIDN:AAA17561.1; PID:g437106
C:Superfamily: rhodopsin kinase; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:184-448/Domain: protein kinase homology <KIN>
F:192-200/Region: protein kinase ATP-binding motif

Query Match 5.8%; Score 7; DB 1; Length 590;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LIQLRFK 52
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Db 550 LIQLRFK 556

Search completed: May 3, 2002, 12:29:12
Job time: 128 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 12:28:49 ; Search time 11.8 Seconds
(without alignments)
375.970 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 121
Sequence: 1 MRIMLLFTAILAFSLAQSG.....DVNQENVPSPGILKYPPRAE 121

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size : 0
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	8.3	116	1	TKNK_MOUSE
2	10	8.3	116	1	TKNK_RAT
3	10	8.3	126	1	TKNK_BOVIN
4	8	6.6	10	1	TKNK_PIG
5	8	6.6	3099	1	POLG_PEMVM
6	7	5.8	310	1	YNOO_MYCTU
7	7	5.8	590	1	GRK5_BOVIN
8	7	5.8	590	1	GRK5_HUMAN
9	7	5.8	648	1	CCMF_HAETN
10	7	5.8	792	1	ATX1_MOUSE
11	6	5.0	63	1	HIG2_HUMAN
12	6	5.0	73	1	SAS2_BACME
13	6	5.0	73	1	SAS5_BACME
14	6	5.0	77	1	Y084_TREPA
15	6	5.0	104	1	YJB8_YEAST
16	6	5.0	108	1	VNBP_PVAG
17	6	5.0	108	1	VNBP_PVMR
18	6	5.0	110	1	Y225_METJA
19	6	5.0	113	1	FRT2_HUMAN
20	6	5.0	126	1	SECG_PSESY
21	6	5.0	130	1	FLHE_ECOLI
22	6	5.0	130	1	FLHE_SALTY
23	6	5.0	141	1	HBAB_RANCA
24	6	5.0	152	1	MYG_APTFO
25	6	5.0	153	1	MYG_HALGR
26	6	5.0	153	1	MYG_PHOSI
27	6	5.0	153	1	MYG_PHYCA
28	6	5.0	154	1	RL2B_TOBAC
29	6	5.0	155	1	VG05_BPML5
30	6	5.0	156	1	CB20_HUMAN
31	6	5.0	160	1	Y650_TREPA
32	6	5.0	162	1	YD73_METJA
33	6	5.0	163	1	COAD_STRPY

168	1	COX2_THETH	P98052	thermus aqu
173	1	TCPA_AMBME	P50157	ambystoma m
183	1	SIEB_LAMBD	P03762	bacterioph
195	1	RAC4_ARATH	Q38919	arabidopsis
196	1	RAC5_ARATH	Q38937	arabidopsis
197	1	RAC1_ARATH	Q38902	arabidopsis
197	1	RAC1_BETVU	Q39435	beta vulgar
201	1	RAC1_PEA	Q35638	pisum sativ
201	1	GLND_SALTY	P23679	salmonella
208	1	Y146_UREPA	Q9p288	ureaplasma
209	1	ENTD_ECOLI	P19225	escherichia
212	1	ER21_BOVIN	P33946	bos taurus
212	1	ER21_HUMAN	P24390	homo sapien
212	1	OSC2_BORBU	Q08137	borrelia bu
220	1	ALKB_CAUCR	Q05725	caulobacter
227	1	UPP_HA1N1	Q9hm05	halobacteri
228	1	ISPD_BACHD	Q9kf88	bacillus ha
239	1	RIM9_YEAST	Q04734	saccharomyc
240	1	UL20_VZVD	P09290	varicella-z
241	1	CL11_HUMAN	O00299	homo sapien
241	1	CL11_MOUSE	Q921q5	mus musculus
245	1	FLIP_ECOLI	P33133	escherichia
245	1	FLIP_SALTY	P54700	salmonella
245	1	GSC_CHICK	P53545	gallus gall
245	1	OCCM_RHIME	P72296	rhizobium m
247	1	RS3_CAEEL	P48152	caenorhabdi
253	1	GS2_HUMAN	P41247	homo sapien
258	1	FLIP_ERWCA	P34200	erwinia car
260	1	CF30_MYCTU	O75822	homo sapien
271	1	YD17_HAETN	O53774	mycobacteri
281	1	NHOA_SALTY	P44160	haemophilus
282	1	LRPR_STREQ	Q00267	salmonella
300	1	NUSG_STRCO	Q54087	streptococc
303	1	NULM_CABUN	P36266	streptomyce
309	1	NUSG_STRGB	O78700	cabassous u
312	1	SNAG_HUMAN	P52852	streptomyce
327	1	CD1A_HUMAN	Q99747	homo sapien
328	1	SNAG_BOVIN	P06126	homo sapien
330	1	C1B4_CAVPO	P81127	bos taurus
331	1	DGAL_HAETN	Q9q2y9	cavia porce
333	1	C1B1_CAVPO	P44883	haemophilus
333	1	CD1B_HUMAN	Q9q222	cavia porce
335	1	CD1D_HUMAN	P29016	homo sapien
335	1	RPC5_YEAST	P15813	homo sapien
335	1	TRPD_BUCDN	P07703	saccharomyc
336	1	CD1D_RAT	O68426	buchnera ap
337	1	ATH2_MOUSE	Q63493	rattus norv
344	1	M1ZD_BACSU	P48986	mus musculus
348	1	GALE_HUMAN	P26935	bacillus su
359	1	AG2R_CANFA	Q14376	homo sapien
359	1	AG2R_MERUN	P43240	canis fami
359	1	AG2R_MOUSE	O35210	meriones un
359	1	AG2R_PIG	P29754	mus musculus
359	1	AG2R_RAT	P30555	sus scrofa
359	1	RECF_DEIRA	P25095	rattus norv
360	1	LPXB_HELPJ	Q9rv00	deinococcu
360	1	LPXB_HELPJ	Q9zky2	helicobacte
361	1	APEA_DICDI	O25537	helicobacte
363	1	HACA_AGRU	P51173	dictyosteli
365	1	YUCL_YEAST	O68443	agrobacteri
366	1	YOP3_CAEEL	P47067	saccharomyc
372	1	HMEN_BOMMO	Q22695	caenorhabdi
377	1	SH1D_CANFA	P27609	bombyx mori
379	1	CYB_FELCA	P11614	canis fami
379	1	CYB_LORTA	P48886	felis silve
387	1	GAT6_CHICK	Q34952	loris tard
388	1	ODPT_HUMAN	P43693	gallus gall
393	1	FMT_YEAST	P29803	homo sapien
395	1	CGA2_CHICK	P32785	saccharomyc
398	1	Y4QJ_RHISN	P43449	gallus gall
399	1	NTG1_YEAST	P55631	rhizobium s
399	1	TCR1_ECOLI	P31378	saccharomyc
399	1	TCR1_ECOLI	P02982	escherichia

107	6	5.0	402	1	KAS2_STRCM	P41176 streptomyc	180	6	5.0	727	1	GPDM_RAT	P35571 rattus norv
108	6	5.0	421	1	FXJ1_MOUSE	Q61560 mus musculu	181	6	5.0	727	1	YR22_CABEL	Q09639 caenorhabdi
109	6	5.0	421	1	FXJ1_RAT	Q63247 rattus norv	182	6	5.0	728	1	SPEI_PEA	Q43075 plium sativ
110	6	5.0	430	1	CLPX_BORBU	O51557 borrelia bu	183	6	5.0	731	1	CATA_HALMA	O59651 haloarcula
111	6	5.0	431	1	CIT1_ECOLI	P07661 escherichia	184	6	5.0	738	1	LDLC_HUMAN	O14746 homo sapien
112	6	5.0	434	1	CIT1_SALTY	P24115 salmonella	185	6	5.0	744	1	GYRA_AQUAE	O67108 aquifex aeo
113	6	5.0	435	1	RUBB_CHLRE	Q42893 chlamydomon	186	6	5.0	746	1	CLC5_MOUSE	P51795 homo sapien
114	6	5.0	443	1	YEY2_YEAST	P10356 saccharomyc	187	6	5.0	746	1	CLC5_MOUSE	Q9WVd4 mus musculu
115	6	5.0	454	1	P2CH_HUMAN	P49593 homo sapien	188	6	5.0	746	1	CLC5_RAT	P51796 rattus norv
116	6	5.0	456	1	PUR1_ARCFU	Q29388 archaeoglob	189	6	5.0	748	1	KLH1_HUMAN	Q9NRt64 homo sapien
117	6	5.0	459	1	ZPR1_HUMAN	O75312 homo sapien	190	6	5.0	779	1	SRP_DROME	P52172 drosophila
118	6	5.0	459	1	ZPR1_MOUSE	Q62384 mus musculu	191	6	5.0	788	1	PAB5_YEAST	P37254 saccharomyc
119	6	5.0	464	1	L2AM_DROME	P18486 drosophila	192	6	5.0	802	1	PEFC_SALTY	P37868 salmonella
120	6	5.0	470	1	CPBK_MOUSE	Q62397 mus musculu	193	6	5.0	804	1	GYRA_THEMEA	O33926 thermotoga
121	6	5.0	479	1	SAHH_PLAF7	P50250 plasmodium	194	6	5.0	810	1	SYEF_SYNY3	P74296 synechocyst
122	6	5.0	481	1	CAP_CHLVR	Q01122 chlorohydra	195	6	5.0	812	1	P3K2_SOYBN	P42348 glycine max
123	6	5.0	484	1	DNAA_ZYMMO	Q9S493 zymomonas m	196	6	5.0	814	1	P3K1_SOYBN	P42347 glycine max
124	6	5.0	491	1	CPB1_RAT	P00176 rattus norv	197	6	5.0	824	1	CC27_HUMAN	P30260 homo sapien
125	6	5.0	491	1	CPB2_RAT	P04167 rattus norv	198	6	5.0	824	1	SYL_THEMEA	Q9WY15 thermotoga
126	6	5.0	491	1	CPB4_RABIT	P00178 oryctolagus	199	6	5.0	831	1	DPO1_THEMEFL	P30313 thermus aqu
127	6	5.0	491	1	CPB5_RABIT	P12789 oryctolagus	200	6	5.0	832	1	DPO1_THEMEA	P19821 thermus aqu
128	6	5.0	491	1	CPB6_HUMAN	P20813 homo sapien	201	6	5.0	853	1	CNRB_BOVIN	P23439 bos taurus
129	6	5.0	491	1	CPB9_MOUSE	P12790 mus musculu	202	6	5.0	854	1	CNRB_HUMAN	P35913 homo sapien
130	6	5.0	492	1	CPBC_RAT	P33272 rattus norv	203	6	5.0	856	1	CNRB_MOUSE	P23440 mus musculu
131	6	5.0	492	1	CPBT_MOUSE	O55071 mus musculu	204	6	5.0	864	1	GYRA_STRCO	P35885 streptomyc
132	6	5.0	492	1	SES1_HUMAN	Q9Y9P5 homo sapien	205	6	5.0	867	1	GLND_KLEPN	P41393 klebsiella
133	6	5.0	492	1	SES1_MOUSE	P58006 mus musculu	206	6	5.0	890	1	BCN5_CLOPE	P08696 clostridium
134	6	5.0	494	1	CPBB_CANFA	P24460 canis famli	207	6	5.0	890	1	GLND_ECOLI	P27249 escherichia
135	6	5.0	500	1	CPBA_MOUSE	P12791 mus musculu	208	6	5.0	895	1	YA54_METJA	O58454 methanococ
136	6	5.0	510	1	FKH_DROME	P14734 drosophila	209	6	5.0	908	1	DPO1_BORBU	O51498 borrelia bu
137	6	5.0	510	1	SYK_SYNY3	P73443 synechocyst	210	6	5.0	932	1	PMS1_HUMAN	P54277 homo sapien
138	6	5.0	512	1	AMT1_DEBOC	P19269 debaryomyc	211	6	5.0	944	1	SUHW_DROME	P08970 drosophila
139	6	5.0	516	1	GUX1_NEUCR	P38676 neurospora	212	6	5.0	989	1	PSD1_CABEL	Q18115 caenorhabdi
140	6	5.0	526	1	IEG3_HSV7J	P52355 human herpe	213	6	5.0	1005	1	EVG_MOUSE	P57680 mus musculu
141	6	5.0	534	1	LY41_STRCO	O86511 streptomyc	214	6	5.0	1018	1	YKC2_CABEL	P41933 caenorhabdi
142	6	5.0	541	1	CH60_EHREQ	O34191 ehrllichia e	215	6	5.0	1021	1	ATN1_CHICK	P09572 gallus gall
143	6	5.0	541	1	CH82_RHOSH	P95847 rhodobacter	216	6	5.0	1063	1	ELF1_DROME	P13002 drosophila
144	6	5.0	545	1	CH60_BORBU	P27575 borrelia bu	217	6	5.0	1101	1	DIA2_HUMAN	Q60879 homo sapien
145	6	5.0	545	1	CH60_PSEPU	P48216 pseudomonas	218	6	5.0	1197	1	Y4CA_RHSIN	P55383 rhizobium s
146	6	5.0	547	1	CH60_BORPE	P48210 bordetella	219	6	5.0	1222	1	YMP3_CABEL	O10947 caenorhabdi
147	6	5.0	547	1	CH60_PSEAE	P30718 pseudomonas	220	6	5.0	1230	1	SMC3_YEAST	P47037 saccharomyc
148	6	5.0	547	1	TCPA_TETPY	O15891 tetrahymena	221	6	5.0	1276	1	MDR1_CRIGR	P21448 cricetus
149	6	5.0	550	1	CH60_EHRC	P42382 ehrllichia c	222	6	5.0	1276	1	MDR2_CRIGR	P21449 cricetus
150	6	5.0	551	1	ASLA_ECOLI	P25549 escherichia	223	6	5.0	1276	1	MDR2_MOUSE	P21440 mus musculu
151	6	5.0	551	1	CH60_COWRU	P48213 cowdria rum	224	6	5.0	1277	1	MDR2_RAT	P43245 rattus norv
152	6	5.0	552	1	CH60_COXBU	P19421 coxiella bu	225	6	5.0	1278	1	MDR2_MOUSE	Q08201 rattus norv
153	6	5.0	552	1	CH60_PSEAT	O33500 pseudomonas	226	6	5.0	1381	1	MDR3_CRIGR	P21374 cricetus
154	6	5.0	553	1	YMB8_YEAST	Q04847 saccharomyc	227	6	5.0	1371	1	VCAP_HSVSA	Q00999 herpesvirus
155	6	5.0	554	1	ATRA_STRCO	Q9X900 streptomyc	228	6	5.0	1387	1	TOP2_PENCH	Q09898 penicillium
156	6	5.0	556	1	TCP1_MOUSE	P11984 mus musculu	229	6	5.0	1630	1	ESPI_YEAST	P02566 saccharomyc
157	6	5.0	556	1	TCP2_MOUSE	P11983 mus musculu	230	6	5.0	1966	1	MYSE_CABEL	P02566 caenorhabdi
158	6	5.0	556	1	TCPA_CRIGR	P18279 cricetus	231	6	5.0	2131	1	YCF2_SPTOL	P08973 spinacia ol
159	6	5.0	556	1	TCPA_HUMAN	P17987 homo sapien	232	6	5.0	2112	1	RRPL_EBOZM	Q05318 ebola virus
160	6	5.0	556	1	TCPA_RAT	P28480 rattus norv	233	6	5.0	2294	1	YCF2_ARATH	P56786 arabidopsis
161	6	5.0	556	1	TCPA_SCHPO	O94501 schizosacch	234	6	5.0	2670	1	YAQ5_SCHPO	Q10105 schizosacch
162	6	5.0	557	1	TCPA_MONDO	Q9XT06 monodelphis	235	6	5.0	2769	1	THYC_BOVIN	P01267 bos taurus
163	6	5.0	559	1	TCPA_PALPA	Q9W790 paleosuchus	236	6	5.0	3421	1	TEGU_HSVBE	P28955 equine herp
164	6	5.0	559	1	TCPA_YEAST	P12612 saccharomyc	237	6	5.0	4499	1	DYHA_CHLRE	Q39610 chlamydomon
165	6	5.0	565	1	UBPN_HUMAN	Q9UK80 homo sapien	238	6	5.0	4	1	TLP_ACTDE	P81370 actinidia d
166	6	5.0	566	1	UBPN_MOUSE	Q9Q216 mus musculu	239	5	4.1	29	1	AP65_CARMA	P82964 carcinus ma
167	6	5.0	570	1	MKS8_HUMAN	Q9NPJ1 homo sapien	240	5	4.1	30	1	PSAN_CVACA	Q9TLX5 cyanidium c
168	6	5.0	570	1	MKS8_MOUSE	Q9J170 mus musculu	241	5	4.1	36	1	RET4_CHICK	P30370 gallus gall
169	6	5.0	575	1	RECU_ERWCH	P39693 erwinia chr	242	5	4.1	43	1	MTA_COLVI	P27086 colinus vir
170	6	5.0	576	1	GRK6_HUMAN	P43250 homo sapien	243	5	4.1	43	1	TKB3_LYCES	P27087 colinus vir
171	6	5.0	576	1	GRK6_MOUSE	O70293 mus musculu	244	5	4.1	44	1	RK32_VICFA	P36493 lycopersic
172	6	5.0	576	1	GRK6_RAT	P97711 rattus norv	245	5	4.1	48	1	RK32_VICFA	P36493 lycopersic
173	6	5.0	628	1	MSLN_HUMAN	Q13421 homo sapien	246	5	4.1	50	1	C555_BACAZ	P23037 bacillus az
174	6	5.0	658	1	DNLJ_MYCPN	P78021 mycoplasma	247	5	4.1	54	1	RK32_TOBAC	P12198 nicotiana t
175	6	5.0	667	1	YFAE_BACSU	P37519 bacillus su	248	5	4.1	56	1	RK32_SPTOL	P28804 spinacia ol
176	6	5.0	695	1	CMC1_DROME	Q9VA73 drosophila	249	5	4.1	59	1	RL37_ARCFU	O29387 archaeoglob
177	6	5.0	695	1	YCX7_CHLUV	O20159 chlorella v	250	5	4.1	60	1	YXBI_BRARE	O42366 brachydanio
178	6	5.0	704	1	YB1_YEAST	P38273 saccharomyc	251	5	4.1	60	1	YXBI_AZOVI	Q44557 azotobacter
179	6	5.0	725	1	VR2A_BPT4	P03690 bacterioph	252	5	4.1	63	1	MT2_COLLI	P15787 columba liv

253	5	4.1	63	1	MT_CHICK	P09576	gallus gall	326	5	4.1	102	1	RS24_AERPE	Q9ycy0	aeropyrum p
254	5	4.1	64	1	Y314_ARCFU	Q29931	archaeoglob	327	5	4.1	105	1	YF40_PYRAB	Q9uz84	pyrococcus
255	5	4.1	64	1	Y975_METJA	Q58385	methanococc	328	5	4.1	106	1	Y368_METJA	Q57814	methanococc
256	5	4.1	64	1	YA74_ARCFU	Q29189	archaeoglob	329	5	4.1	106	1	Y547_RICPR	Q92d03	rickettsia
257	5	4.1	65	1	YCF9_EUGGR	P32095	euglena gra	330	5	4.1	106	1	Y891_YEAST	P38341	saccharomyc
258	5	4.1	68	1	RK32_MARPO	P12196	marichantia	331	5	4.1	106	1	YCPW_PSEA9	P29298	pseudanabae
259	5	4.1	69	1	RK32_PINTH	P41651	pinus thunb	332	5	4.1	107	1	GUAN_CAMPO	P06664	cavia porce
260	5	4.1	70	1	YVAK_VACCC	P20520	vaccinia vi	333	5	4.1	107	1	VLYS_LAMBD	P03705	bacterioph
261	5	4.1	71	1	FBS_ONCMY	Q60791	mus musculu	334	5	4.1	107	1	YK9_YEAST	P53138	saccharomyc
262	5	4.1	71	1	G0N3_ONCMY	P55246	oncorhynch	335	5	4.1	108	1	ATPR_BOVIN	P02721	bos taurus
263	5	4.1	74	1	G0N3_ONCTS	Q92097	oncorhynch	336	5	4.1	108	1	ATPR_HUMAN	P18859	homo sapien
264	5	4.1	75	1	VGE_BPPHK	Q38040	bacterioph	337	5	4.1	108	1	HEMA_IARI5	P03450	influenza a
265	5	4.1	77	1	RS9_TOBAC	P49214	nicotiana t	338	5	4.1	108	1	SY19_MOUSE	O70460	mus musculu
266	5	4.1	77	1	VG43_BPMLS	Q05255	mycobacteri	339	5	4.1	108	1	VLY1_BPP22	P09962	bacterioph
267	5	4.1	78	1	GVPA_HALME	P23761	halobacteri	340	5	4.1	108	1	YD08_METJA	Q58704	methanococc
268	5	4.1	79	1	AKHD_DROME	P17975	drosophila	341	5	4.1	109	1	SYR_STRPN	Q54869	streptococc
269	5	4.1	79	1	ATP9_ACACA	Q37377	acanthamoeb	342	5	4.1	109	1	YF79_MYCPN	P55201	mycoplasma
270	5	4.1	79	1	ET2_WACFA	Q28470	macaca fasc	343	5	4.1	110	1	RLA4_YEAST	P02400	saccharomyc
271	5	4.1	80	1	PE_RAT	Q54842	rattus norv	344	5	4.1	111	1	ARPP_BOVIN	Q28055	bos taurus
272	5	4.1	81	1	ATPL_CLOAB	O08310	clostridium	345	5	4.1	111	1	ARPP_HUMAN	P56211	homo sapien
273	5	4.1	81	1	YQGY_BACSU	P54502	bacillus su	346	5	4.1	111	1	ARPP_MOUSE	P56212	mus musculu
274	5	4.1	81	1	G0N3_ONCMA	P30973	oncorhynch	347	5	4.1	111	1	OL7H_MOUSE	Q60893	mus musculu
275	5	4.1	82	1	G0N3_SALSA	P35629	salmo salar	348	5	4.1	111	1	SC4_SCHCO	P16934	schizophyll
276	5	4.1	82	1	G0N3_SALTR	P45653	salmo trutt	349	5	4.1	111	1	Y546_SANY3	Q55397	synecocyst
277	5	4.1	82	1	RANA_RANPI	P08950	rana pipien	350	5	4.1	111	1	YDR3_SCHPO	O13738	schizosacch
278	5	4.1	82	1	RR16_PORPU	P11352	porphyra pu	351	5	4.1	112	1	FLIN_AQUAE	O67495	aquifex aeo
279	5	4.1	83	1	SEEP_RAPSA	P11573	raphanus sa	352	5	4.1	113	1	DAD1_CAEEL	P52872	caenorhabdi
280	5	4.1	84	1	GLRX_PSEAE	Q9hu55	pseudomonas	353	5	4.1	113	1	RAMA_ENTCL	P55922	enterobacte
281	5	4.1	84	1	Y519_METJA	Q57939	methanococc	354	5	4.1	113	1	RAMA_KLEPN	Q48413	klebsiella
282	5	4.1	84	1	Y296_HAEIN	P44220	haemophilus	355	5	4.1	114	1	RL19_SALTY	P36240	salmonella
283	5	4.1	86	1	YVAB_VACCC	P20511	vaccinia vi	356	5	4.1	114	1	SMSA_CARAU	Q9ygh5	carassius a
284	5	4.1	87	1	BXBA_BOMMO	Q17194	bombyx mori	357	5	4.1	114	1	YFEC_ECOLI	P27239	escherichia
285	5	4.1	87	1	RS21_NEUCR	Q93798	neurospora	358	5	4.1	114	1	YGI3_BACTU	P10024	bacillus th
286	5	4.1	88	1	RL31_SULSO	P58190	sulfolobus	359	5	4.1	115	1	MOTI_BOVIN	O62820	bos taurus
287	5	4.1	89	1	G0N3_PORNO	P51922	porichthys	360	5	4.1	115	1	MOTI_HUMAN	P12872	homo sapien
288	5	4.1	90	1	DBHA_AERHY	Q91a96	aeromonas h	361	5	4.1	115	1	MOTI_MACMU	O18811	macaca mula
289	5	4.1	90	1	G0N3_DICLA	Q91a09	dicentrarch	362	5	4.1	115	1	MOTI_SHEEP	O18845	ovis aries
290	5	4.1	90	1	G0N3_HAPBU	P45652	haplochromi	363	5	4.1	115	1	PSBW_PORPU	P51347	porphyra pu
291	5	4.1	90	1	G0N3_PAGNA	P51921	pagrus maj	364	5	4.1	115	1	RL19_HAEIN	P44357	haemophilus
292	5	4.1	90	1	G0N3_SPAAU	P51923	sparus aur	365	5	4.1	115	1	RL20_BORBU	O51206	borrelia bu
293	5	4.1	91	1	EMB5_MAIZE	P46517	zea mays (m	366	5	4.1	115	1	SMS1_PROAN	Q9w7f0	prototeterus
294	5	4.1	91	1	EML_PICGL	Q40864	picea glauc	367	5	4.1	116	1	MOTI_FELCA	Q9xse2	felis silve
295	5	4.1	92	1	EM6_ARATH	O02973	arabidopsis	368	5	4.1	116	1	Y157_AQUAE	O67709	aquifex aeo
296	5	4.1	92	1	EMB1_DAUCA	P17639	daucus caro	369	5	4.1	118	1	LTP5_ARATH	Q9xf57	arabidopsis
297	5	4.1	92	1	G0N1_CHICK	P37042	gallus gall	370	5	4.1	118	1	YGI3_YEAST	P53231	saccharomyc
298	5	4.1	92	1	LE10_HELAN	P46514	helianthus	371	5	4.1	120	1	LIPB_PROHO	Q51854	prochloroth
299	5	4.1	92	1	MOTI_HORSE	O46617	equus cabal	372	5	4.1	120	1	NU3C_WHEAT	P26303	tritium ae
300	5	4.1	92	1	PTSO_VIBCH	Q9kp46	vibrio chol	373	5	4.1	120	1	RET3_CHICK	P40220	gallus gall
301	5	4.1	93	1	EM1_WHEAT	P04568	tritium ae	374	5	4.1	120	1	VGB_BPG4	P03634	bacterioph
302	5	4.1	93	1	EM3_WHEAT	Q08000	tritium ae	375	5	4.1	121	1	SRI4_ARATH	O04421	arabidopsis
303	5	4.1	93	1	EM4_WHEAT	P42755	tritium ae	376	5	4.1	122	1	Y16A_UREPA	Q9pqx8	ureaplasma
304	5	4.1	93	1	GATC_HELPF	Q92km6	helicobacte	377	5	4.1	122	1	YJ16_YEAST	P47028	saccharomyc
305	5	4.1	93	1	GATC_HELPF	O25626	helicobacte	378	5	4.1	123	1	YXG6_YEAST	P53077	saccharomyc
306	5	4.1	93	1	L19A_HORVU	Q05190	hordeum vul	379	5	4.1	124	1	COX4_SAISS	O46582	saimiri sci
307	5	4.1	93	1	L19B_HORVU	P46532	hordeum vul	380	5	4.1	125	1	LECC_POLMI	P16108	polyandroca
308	5	4.1	93	1	Y292_METJA	Q57740	methanococc	381	5	4.1	125	1	NEUM_BUFJA	P08162	bufo japoni
309	5	4.1	93	1	Y008_BPHF1	P51709	bacterioph	382	5	4.1	125	1	YBAN_ECOLI	P45808	escherichia
310	5	4.1	94	1	EM2_WHEAT	P22701	tritium ae	383	5	4.1	125	1	YM88_MYCTU	Q50677	mycobacteri
311	5	4.1	94	1	G0N3_CARAU	P51917	carassius a	384	5	4.1	126	1	MSP2_ASCSU	P27440	ascaris suu
312	5	4.1	94	1	G0N3_RUTRU	Q92106	rutilus rut	385	5	4.1	126	1	WN72_EPTST	P28123	epitretus
313	5	4.1	94	1	N18M_NEUCR	Q07842	neurospora	386	5	4.1	127	1	YBBA_BACSU	P55192	bacillus su
314	5	4.1	95	1	EMPI_ORISA	P46520	oryza sativ	387	5	4.1	128	1	AR21_ENTHI	O15604	chromoeba h
315	5	4.1	96	1	Y1B3_CLOAB	P34159	clostridium	388	5	4.1	128	1	PHE3_CHRSP	Q00433	entamoeba h
316	5	4.1	97	1	YQ1H_BACSU	P40770	bacillus su	389	5	4.1	129	1	NKL_PIG	P29075	sus scrofa
317	5	4.1	99	1	YD60_METJA	Q58755	methanococc	390	5	4.1	129	1	TKN1_HUMAN	Q20366	homo sapien
318	5	4.1	100	1	URE3_ECOLI	Q03282	escherichia	391	5	4.1	130	1	TKN1_BOVIN	P01289	bos taurus
319	5	4.1	100	1	URE3_KLEAE	P18316	klebsiella	392	5	4.1	130	1	TKN1_MESAU	Q60541	mesocricetu
320	5	4.1	100	1	URE3_KLEPN	Q02943	klebsiella	393	5	4.1	130	1	TKN1_MOUSE	P41539	mus musculu
321	5	4.1	100	1	URE3_PROMI	P17088	proteus mir	394	5	4.1	130	1	TKN1_RAT	P06767	rattus norv
322	5	4.1	100	1	URE3_PROVU	P16124	proteus vul	395	5	4.1	131	1	BACH_HALAR	Q53461	haloaula
323	5	4.1	101	1	PRG1_SALTY	P41785	salmonella	396	5	4.1	131	1	SODN_STRCO	P80735	streptomyce
324	5	4.1	102	1	LE19_GOSHI	P09443	gossypium h	397	5	4.1	131	1	ULC7_HCMVA	P16771	human cytom
325	5	4.1	102	1	MGN_ORISA	P49030	oryza sativ	398	5	4.1	131	1	YJ56_VIBCH	Q9kv02	vibrio chol

399	5	4.1	133	1	L193_HORVU	Q02400 hordeum vul	472	5	4.1	168	1	NU6M_DIDMA	P41315 didelphis m
400	5	4.1	133	1	R24B_SCHPO	O59865 schizosacch	473	5	4.1	168	1	YEW1_HAEIN	P44217 haemophilus
401	5	4.1	134	1	LEGI_BUFAR	P56217 bufo arenar	474	5	4.1	168	1	YEW1_CAEEL	Q11088 caenorhabdi
402	5	4.1	135	1	JANA_DROME	P20348 drosophila	475	5	4.1	169	1	RIMM_NEIMA	Q9JVK9 neisseria m
403	5	4.1	135	1	Y4PE_RHISN	P55614 rhizobium s	476	5	4.1	169	1	RIMM_NEIMB	Q9KOK3 neisseria m
404	5	4.1	136	1	RET3_BOVIN	P02695 bos taurus	477	5	4.1	172	1	MBEE_ECOLI	P13659 escherichia
405	5	4.1	136	1	RET3_FUGRU	O42386 fugu rubrip	478	5	4.1	172	1	Y427_UREUR	Q56364 ureaplasma
406	5	4.1	136	1	RET3_HUMAN	P29762 homo sapien	479	5	4.1	173	1	SODC_PHOLE	P00446 photobacter
407	5	4.1	137	1	YUXK_BACSU	P40761 bacillus su	480	5	4.1	173	1	SODC_PHOLE	P00446 photobacter
408	5	4.1	137	1	DIU1_MANSE	P21819 manduca sex	481	5	4.1	174	1	AX12_ARATH	P49678 arabidopsis
409	5	4.1	138	1	TEPD_ECOLI	P28816 escherichia	482	5	4.1	174	1	YA68_METTH	O27140 methanobact
410	5	4.1	139	1	GALE_KLEPN	P45602 klebsiella	483	5	4.1	175	1	CPCS_CANPG	P81584 cancer pagu
411	5	4.1	139	1	YU06_YEAST	P53842 saccharomyc	484	5	4.1	175	1	RBS_CAMJE	Q38793 aegilops ta
412	5	4.1	140	1	IL4_MOUSE	P07750 mus musculu	485	5	4.1	176	1	NOOA_THETH	O9ppe0 campylobact
413	5	4.1	141	1	HBA2_HORSE	P13787 equus cabal	486	5	4.1	176	1	OMLA_PSEAE	O56225 thermus aqu
414	5	4.1	142	1	Y213_AQUAE	O50813 mycobacteri	487	5	4.1	177	1	3HAO_YEAST	O68562 pseudomonas
415	5	4.1	142	1	AT92_BOVIN	P06406 aquifex aeo	488	5	4.1	177	1	COX2_RICPR	P47096 saccharomyc
416	5	4.1	143	1	AT92_BOVIN	P07926 bos taurus	489	5	4.1	178	1	ET2_HUMAN	Q92dm3 rickettsia
417	5	4.1	143	1	AT92_SHEEP	Q06056 ovis aries	490	5	4.1	178	1	EAR_ASPB7	P20800 homo sapien
418	5	4.1	143	1	YU03_CHLMU	O9plu2 chlamydia m	491	5	4.1	179	1	EAR_ASPB7	P42485 african swi
419	5	4.1	144	1	COX4_AOTAZ	O46584 aotus azara	492	5	4.1	179	1	EAR_ASPB7	P42485 african swi
420	5	4.1	144	1	COX4_PITPI	O46585 pithecia pi	493	5	4.1	179	1	EAR_ASPB7	P42485 african swi
421	5	4.1	144	1	HAP3_YEAST	P13434 saccharomyc	494	5	4.1	179	1	SP17_MONDO	O62771 monodelphis
422	5	4.1	144	1	MACH_STRMA	P01549 streptomyc	495	5	4.1	180	1	YPOL_THEFL	P32438 thermus aqu
423	5	4.1	145	1	V341_BPMD2	O64228 mycobacteri	496	5	4.1	180	1	RG88_HUMAN	P57771 homo sapien
424	5	4.1	146	1	AIF1_PIG	P81076 sus scrofa	497	5	4.1	180	1	RG88_HUMAN	P49804 rattus norv
425	5	4.1	146	1	SG50_RAT	Q04807 rattus norv	498	5	4.1	180	1	RL5_SYNY3	P73308 synchocyst
426	5	4.1	146	1	YAT7_SCHPO	O10152 schizosacch	499	5	4.1	181	1	SMCX_CRIGR	P41228 cricetus
427	5	4.1	146	1	YN81_YEAST	P40342 saccharomyc	500	5	4.1	181	1	Y422_CHLPN	Q928c1 chlamydia p
428	5	4.1	147	1	AIF1_HUMAN	P55008 homo sapien	501	5	4.1	182	1	RL5_SULSO	O9ux93 sulfolobus
429	5	4.1	147	1	AIF1_RAT	P55009 rattus norv	502	5	4.1	183	1	YG2R_YEAST	P53260 saccharomyc
430	5	4.1	147	1	U441_HVMG	Q05105 marek's dis	503	5	4.1	184	1	ATPD_SYNP1	Q05374 synchococ
431	5	4.1	148	1	PFDA_PYRAB	O9uyv14 pyrococ	504	5	4.1	184	1	YKWC_BACSU	P45870 bacillus su
432	5	4.1	149	1	RS19_MYAAR	O94613 mya arenari	505	5	4.1	185	1	END4_BPT4	P39250 bacterioph
433	5	4.1	150	1	YE42_MYCPN	P75336 mycoplasma	506	5	4.1	185	1	RP06_MYXVA	P18620 myxoma viru
434	5	4.1	151	1	SM03_DROME	Q04437 drosophila	507	5	4.1	185	1	RS9_DICDI	P14132 dictyosteli
435	5	4.1	152	1	EMI_ARATH	O07187 arabidopsis	508	5	4.1	185	1	YPJA_BACSU	P54392 bacillus su
436	5	4.1	152	1	YCF8_YEAST	P25585 saccharomyc	509	5	4.1	186	1	DH18_ARATH	P30185 arabidopsis
437	5	4.1	152	1	YGSF_YEAST	P53328 saccharomyc	510	5	4.1	186	1	GDAB_WHEAT	P04728 triticum ae
438	5	4.1	153	1	L194_HORVU	O05191 hordeum vul	511	5	4.1	186	1	TSBE_HALN1	Q25555 naegleria f
439	5	4.1	154	1	RL2B_FRIAG	O22644 fritillaria	512	5	4.1	186	1	YP89_CAEEL	Q9h556 halobacteri
440	5	4.1	154	1	SODC_PINSY	P24569 pinus sylve	513	5	4.1	188	1	RL5_AQUAE	O09227 caenorhabdi
441	5	4.1	155	1	RLH3_AERPE	Q9YB50 aeropyrum p	514	5	4.1	188	1	RL5_AQUAE	O67568 aquifex aeo
442	5	4.1	156	1	RHML_HUMAN	P25800 homo sapien	515	5	4.1	188	1	YBGD_ECOLI	Q92140 aquifex pyr
443	5	4.1	158	1	ATPD_KLULA	P78700 kluyveromyc	516	5	4.1	189	1	AX13_ARATH	P37909 escherichia
444	5	4.1	158	1	YN55_YEAST	P38875 saccharomyc	517	5	4.1	189	1	AX14_PEA	Q38822 arabidopsis
445	5	4.1	159	1	FUT2_RAT	Q10984 rattus norv	518	5	4.1	189	1	NC51_SCHPO	P49679 pisum sativ
446	5	4.1	159	1	MPA1_CARBE	P38949 carpinus be	519	5	4.1	190	1	GCH1_RICPR	O09711 schizosacch
447	5	4.1	159	1	MPA2_CORAV	Q08407 corylius ave	520	5	4.1	190	1	MOBA_RHOCA	Q92de8 rickettsia
448	5	4.1	159	1	MPAG_ALNGL	P38948 alnus glut	521	5	4.1	190	1	RL5_METJA	Q9x7k0 rhodobacter
449	5	4.1	159	1	RL22_THEMA	P38511 thermotoga	522	5	4.1	190	1	RS9A_SCHPO	P54040 methanococ
450	5	4.1	160	1	ATPD_YEAST	Q12165 saccharomyc	523	5	4.1	190	1	CLJUS_MESAU	O09757 schizosacch
451	5	4.1	160	1	NUOE_AQUAE	O66842 aquifex aeo	524	5	4.1	191	1	CLJUS_MESAU	P52810 podospira a
452	5	4.1	161	1	TBA_LVTPI	P02553 lytechinus	525	5	4.1	191	1	RL5_MICLU	P14683 mesocricetu
453	5	4.1	163	1	ATPF_BACFI	P22481 bacillus fi	526	5	4.1	191	1	RNH2_CAMJE	P33098 micrococcu
454	5	4.1	163	1	CD32_HUMAN	P20963 homo sapien	527	5	4.1	191	1	RS9B_SCHPO	O9pja1 campylobact
455	5	4.1	163	1	IF5A_NEUCR	P38672 neurospora	528	5	4.1	191	1	GIDB_MYCGE	O59675 schizosacch
456	5	4.1	163	1	LSPA_HELPJ	Q9zm73 helicobacte	529	5	4.1	192	1	LPCA_HELPY	P47620 mycoplasma
457	5	4.1	164	1	2SS3_ARATH	P15459 arabidopsis	530	5	4.1	192	1	TRPG_SERMA	O25528 helicobacte
458	5	4.1	164	1	CD32_MOUSE	P24161 mus musculu	531	5	4.1	192	1	AX2D_PHAUA	P00900 serratia ma
459	5	4.1	164	1	YPM1_RHIME	P82891 drosophila	532	5	4.1	193	1	INF1_CHICK	O24542 phaseolus a
460	5	4.1	164	1	YPM1_RHIME	P28953 rhizobium m	533	5	4.1	193	1	INF3_CHICK	P42165 gallus gall
461	5	4.1	165	1	GA45_HUMAN	P24522 homo sapien	534	5	4.1	193	1	Y226_AQUAE	O66417 gallus aeo
462	5	4.1	165	1	MLCH_RAT	P25855 arabidopsis	535	5	4.1	194	1	ACPD_HAEIN	P43013 haemophilus
463	5	4.1	165	1	SPRT_ECOLI	P14200 rattus norv	536	5	4.1	194	1	TRPG_HELPY	O25868 helicobacte
464	5	4.1	165	1	CD32_SHEEP	P39902 escherichia	537	5	4.1	194	1	VMA2_HRSVA	P04545 human respi
465	5	4.1	166	1	GCSI_ARATH	P29329 ovis aries	538	5	4.1	194	1	Y187_RICPR	Q9xdx7 rickettsia
466	5	4.1	166	1	MLCH_MOUSE	Q91q10 arabidopsis	539	5	4.1	196	1	AX2B_PHAUA	P32294 phaseolus a
467	5	4.1	166	1	MLCH_MOUSE	P56942 mus musculu	540	5	4.1	196	1	CAGS_HELPY	P97227 helicobacte
468	5	4.1	167	1	DYN_ENTFC	P00380 enterococcu	541	5	4.1	196	1	CH19_DROGR	P13427 drosophila
469	5	4.1	167	1	NU6M_MACRO	P92670 macropus ro	542	5	4.1	196	1	NTPC_ENTHR	P43436 enterococcu
470	5	4.1	168	1	AX11_ARATH	P49677 arabidopsis	543	5	4.1	196	1	RAC2_LOTJA	Q40220 lotus japon
471	5	4.1	168	1	N1RH_PSEST	Q52525 pseudomonas	544	5	4.1	196	1	RAC9_GOSHI	Q41254 gossypium h

545	1	196	4.1	5	618	Q41253	gossypium h
546	1	197	4.1	5	619	P12543	plasmidium
547	1	198	4.1	5	620	P04656	cavia porce
548	1	198	4.1	5	621	P43732	haemophilus
549	1	198	4.1	5	622	Q9ubm1	homo sapien
550	1	198	4.1	5	623	Q61907	mus musculus
551	1	198	4.1	5	624	Q08388	rattus norv
552	1	198	4.1	5	625	Q08912	arabidopsis
553	1	198	4.1	5	626	Q03673	saccharomyc
554	1	199	4.1	5	627	P24876	ascaris suu
555	1	199	4.1	5	628	Q92lu4	helicobacte
556	1	199	4.1	5	629	Q46897	escherichia
557	1	199	4.1	5	630	P32160	escherichia
558	1	200	4.1	5	631	P27058	lycopersico
559	1	200	4.1	5	632	Q83687	treponema p
560	1	201	4.1	5	633	P94975	mycobacteri
561	1	201	4.1	5	634	Q38903	arabidopsis
562	1	201	4.1	5	635	P54291	pseudomonas
563	1	201	4.1	5	636	Q9kst3	vibrio chol
564	1	201	4.1	5	637	Q03629	saccharomyc
565	1	201	4.1	5	638	P25245	tomato ring
566	1	202	4.1	5	639	P27597	canis fami
567	1	202	4.1	5	640	Q9cc22	mycobacteri
568	1	202	4.1	5	641	P45627	nicotiana t
569	1	202	4.1	5	642	P45642	mycoplasma
570	1	202	4.1	5	643	P08671	rabies viru
571	1	203	4.1	5	644	O24543	phaseolus a
572	1	203	4.1	5	645	P46088	omnastreph
573	1	203	4.1	5	646	P52474	human herpe
574	1	204	4.1	5	647	P53764	bovine herp
575	1	204	4.1	5	648	O84860	chlamydia t
576	1	205	4.1	5	649	P11825	human adeno
577	1	205	4.1	5	650	Q61160	mus musculus
578	1	205	4.1	5	651	P39311	escherichia
579	1	205	4.1	5	652	Q59071	methanococc
580	1	206	4.1	5	653	P29020	mus musculus
581	1	206	4.1	5	654	Q92203	emericella
582	1	206	4.1	5	655	P41128	brassica na
583	1	206	4.1	5	656	P41129	brassica na
584	1	206	4.1	5	657	P41127	arabidopsis
585	1	206	4.1	5	658	P35723	saccharomyc
586	1	207	4.1	5	659	Q9v1y5	pyrococcus
587	1	207	4.1	5	660	Q60771	mus musculus
588	1	207	4.1	5	661	P44858	haemophilus
589	1	207	4.1	5	662	Q51790	pseudomonas
590	1	207	4.1	5	663	P24206	escherichia
591	1	208	4.1	5	664	P17403	sus scrofa
592	1	208	4.1	5	665	Q01580	sus scrofa
593	1	208	4.1	5	666	P26892	bos taurus
594	1	208	4.1	5	667	P41683	felis silve
595	1	208	4.1	5	668	Q49135	methylobact
596	1	208	4.1	5	669	P25532	escherichia
597	1	210	4.1	5	670	Q09790	schizosacch
598	1	210	4.1	5	671	Q9x0d7	thermotoga
599	1	210	4.1	5	672	P27654	saccharomyc
600	1	211	4.1	5	673	O75333	homo sapien
601	1	211	4.1	5	674	Q8520	escherichia
602	1	211	4.1	5	675	O28047	archaeoglob
603	1	213	4.1	5	676	P36586	schizosacch
604	1	213	4.1	5	677	P22573	herpesvirus
605	1	213	4.1	5	678	Q04704	canine ente
606	1	214	4.1	5	679	P11826	human adeno
607	1	214	4.1	5	680	P29908	paracoccus
608	1	215	4.1	5	681	Q54769	synechococc
609	1	215	4.1	5	682	P35924	lactobacill
610	1	216	4.1	5	683	P10957	escherichia
611	1	216	4.1	5	684	O66076	treponema p
612	1	216	4.1	5	685	Q78310	arabidopsis
613	1	216	4.1	5	686	Q57900	arabidopsis
614	1	217	4.1	5	687	O88080	streptomyc
615	1	217	4.1	5	688	Q45461	bacillus su
616	1	217	4.1	5	689	O34878	bacillus su
617	1	217	4.1	5	690	P19416	human adeno
P43786	haemophilus						
P47123	saccharomyc						
P55799	escherichia						
P19169	euglena gra						
Q92d96	rickettsia						
Q10932	caenorhabdi						
P28981	equine herp						
Q09676	schizosacch						
P04904	rattus norv						
P30115	mus musculus						
P40555	saccharomyc						
P03048	bacterioph						
P37678	escherichia						
P32188	esox lucius						
P14312	rhizobium l						
P82474	zingiber of						
Q59240	bacillus st						
Q28035	bos taurus						
P08363	homo sapien						
P51781	sus scrofa						
P09210	homo sapien						
Q16772	homo sapien						
Q9xsg6	equus cabal						
P32897	saccharomyc						
Q61878	mus musculus						
Q08963	oryctolagus						
Q83453	porcine ade						
P03205	epstein-bar						
Q14488	homo sapien						
Q92447	pichia past						
Q9hnu2	halobacteri						
O05756	mycobacteri						
P71841	mycobacteri						
P39135	bacillus su						
O05494	bacillus su						
P25960	escherichia						
Q9rhx0	corynebacte						
P41291	balanopter						
P10000	o corticotr						
P45755	aetomonas h						
O75360	homo sapien						
P13046	nicotiana t						
P07052	nicotiana t						
P11019	bos taurus						
P36543	homo sapien						
Q9sr72	arabidopsis						
Q9xf58	bacillus na						
P36323	equine herp						
P42696	homo sapien						
O83203	treponema p						
O28812	archaeoglob						
O57140	haemophilus						
P50518	mus musculus						
P27330	lilly sympto						
P31773	haemophilus						
Q01387	neurospora						
P49784	bacillus su						
Q01074	bacterioph						
O06906	argyria pseu						
P45148	haemophilus						
Q00595	pseudomonas						
P46641	zea mays (m						
P12312	oryza sativ						
P25411	tritium ae						
P26867	marchantia						
P05828	escherichia						
O51146	borrelia bu						
Q9xiu0	thermotoga						
O81235	arabidopsis						
Q94465	dictyosteli						
P46486	flavaria tr						
P14183	haemophilus						
1	YBN_HAEIN	217	4.1	5	618	Q41253	gossypium h
1	MOGL_YEAST	218	4.1	5	619	P12543	plasmidium
1	RR2_ECOLI	218	4.1	5	620	P04656	cavia porce
1	RR3_EUGR	218	4.1	5	621	P43732	haemophilus
1	Y1363_RICPR	218	4.1	5	622	Q9ubm1	homo sapien
1	YT22_CAEEL	218	4.1	5	623	Q61907	mus musculus
1	VT22_HSVB	219	4.1	5	624	Q08388	rattus norv
1	VG15_HSVB	219	4.1	5	625	Q08912	arabidopsis
1	YA03_SCHPO	219	4.1	5	626	Q03673	saccharomyc
1	GTC1_RAT	220	4.1	5	627	P24876	ascaris suu
1	GTC2_RAT	220	4.1	5	628	Q92lu4	helicobacte
1	GTC_MOUSE	220	4.1	5	629	Q46897	escherichia
1	PSD9_YEAST	220	4.1	5	630	P32160	escherichia
1	RP28_BPSP1	220	4.1	5	631	P27058	lycopersico
1	SGBH_ECOLI	220	4.1	5	632	Q83687	treponema p
1	EPD_ESOLI	220	4.1	5	633	P94975	mycobacteri
1	FIXW_RHILE	221	4.1	5	634	Q38903	arabidopsis
1	GRPE_BACST	221	4.1	5	635	P54291	pseudomonas
1	GTAL_BOVIN	221	4.1	5	636	Q9kst3	vibrio chol
1	GTAL_HUMAN	221	4.1	5	637	Q03629	saccharomyc
1	GTAL_PIG	221	4.1	5	638	P25245	tomato ring
1	GTAL_HUMAN	221	4.1	5	639	P27597	canis fami
1	GTAL_HUMAN	221	4.1	5	640	Q9cc22	mycobacteri
1	GTAL_HUMAN	222	4.1	5	641	P45627	nicotiana t
1	GTAL_HUMAN	222	4.1	5	642	P45642	mycoplasma
1	IM2A_HORSE	222	4.1	5	643	P08671	rabies viru
1	IM23_YEAST	222	4.1	5	644	O24543	phaseolus a
1	EMBP_MOUSE	223	4.1	5	645	P46088	omnastreph
1	HEX8_ADEP3	223	4.1	5	646	P52474	human herpe
1	YL2_EBV	223	4.1	5	647	P53764	bovine herp
1	FXGC_HUMAN	224	4.1	5	648	O84860	chlamydia t
1	HIS7_PICPA	224	4.1	5	649	P11825	human adeno
1	PURQ_HALNI	224	4.1	5	650	Q61160	mus musculus
1	PURQ_MYCLE	224	4.1	5	651	P39311	escherichia
1	PURQ_MYCTU	224	4.1	5	652	Q59071	methanococc
1	SPC_BACSU	224	4.1	5	653	P29020	mus musculus
1	YDHC_BACSU	224	4.1	5	654	Q92203	emericella
1	LEP4_ECOLI	225	4.1	5	655	P41128	brassica na
1	PURQ_CORAM	225	4.1	5	656	P41129	brassica na
1	ATP6_BALMU	226	4.1	5	657	P41127	arabidopsis
1	COLI_ONCKE	226	4.1	5	658	P35723	saccharomyc
1	GSBP_AERHY	226	4.1	5	659	Q9v1y5	pyrococcus
1	PHL1_HUMAN	226	4.1	5	660	Q60771	mus musculus
1	PRR1_TOBAC	226	4.1	5	661	P44858	haemophilus
1	PRR2_TOBAC	226	4.1	5	662	Q51790	pseudomonas
1	VATE_BOVIN	226	4.1	5	663	P24206	escherichia
1	VATE_HUMAN	226	4.1	5	664	P17403	sus scrofa
1	GL32_ARATH	227	4.1	5	665	Q01580	sus scrofa
1	PURQ_BACHD	227	4.1	5	666	P26892	bos taurus
1	VG15_HSVL	227	4.1	5	667	P41683	felis silve
1	Y117_HUMAN	227	4.1	5	668	Q49135	methylobact
1	Y173_TREPA	227	4.1	5	669	P25532	escherichia
1	YE60_ARCFU	227	4.1	5	670	Q09790	schizosacch
1	NEUA_HAEIN	228	4.1	5	671	Q9x0d7	thermotoga

691	5	4.1	233	1	RECO_PSEAE	Q9xcx7 pseudomonas	764	5	4.1	253	1	CIOB_RAT	P31721 rattus norv
692	5	4.1	233	1	R63_BUCAI	P57585 buchnera ap	765	5	4.1	253	1	TA4_EIMTE	P13399 eimeria ten
693	5	4.1	233	1	TL16_ARATH	O22773 arabidopsis	766	5	4.1	253	1	TRPA_LACLA	Q01997 lactococcus
694	5	4.1	234	1	AOX2_AERPE	O9vdx7 aeropyrum p	767	5	4.1	254	1	YK07_CAEEL	P34295 caenorhabd1
695	5	4.1	234	1	GCH1_SYNY3	Q55759 synechocyst	768	5	4.1	255	1	DLX1_MOUSE	O64317 mus musculu
696	5	4.1	234	1	TFD2_ALCEU	P42428 alcaligenes	769	5	4.1	255	1	QCR_CACSU	P46913 bacillus su
697	5	4.1	234	1	YMF6_ECOLI	P75968 escherichia	770	5	4.1	256	1	HC_MOUSE	Q02591 mus musculu
698	5	4.1	235	1	RGS1_MOUSE	Q99pg4 mus musculu	771	5	4.1	256	1	GM34_CAEEL	Q94165 caenorhabd1
699	5	4.1	236	1	H1S4_RHOCA	O30725 rhodobacter	772	5	4.1	256	1	HYPB_HYPLI	P35588 hypoderma 1
700	5	4.1	236	1	NUOC_MYCTU	P95179 mycobacteri	773	5	4.1	256	1	PDX3_HUMAN	P35048 homo sapien
701	5	4.1	236	1	TENA_BACSU	P25052 bacillus su	774	5	4.1	256	1	UPPS_BACHD	O9ka67 bacillus ha
702	5	4.1	237	1	H1S4_METJA	Q58927 methanococc	775	5	4.1	256	1	VATD_YEAST	P32610 saccharomyc
703	5	4.1	237	1	LPXH_HAEIN	P44046 haemophilus	776	5	4.1	256	1	YOEU_BACSU	P54461 bacillus su
704	5	4.1	237	1	R33A_HUMAN	Q14088 homo sapien	777	5	4.1	257	1	FMB1_BACNO	P17834 bacteroides
705	5	4.1	237	1	R33A_MOUSE	P97950 mus musculu	778	5	4.1	257	1	FMBX_BACNO	P27905 bacteroides
706	5	4.1	237	1	YB39_MYCPN	P75339 mycoplasma	779	5	4.1	257	1	ICEP_MOUSE	O89094 mus musculu
707	5	4.1	238	1	CHV1_RHISN	P50351 rhizobium s	780	5	4.1	257	1	NOCP_AGRTU	P35116 agrobacteri
708	5	4.1	238	1	YATF_RHISN	P55660 rhizobium s	781	5	4.1	257	1	VATD_CAEEL	P34462 caenorhabd1
709	5	4.1	239	1	CENB_SHEEP	P94511 ovis aries	782	5	4.1	257	1	YGB5_BPNF	P11186 bacterioph
710	5	4.1	239	1	RNC_HELPJ	Q921h2 helicobacte	783	5	4.1	257	1	YGBF_BACSU	O34447 bacillus su
711	5	4.1	239	1	SFSA_RHIME	O87322 rhizobium m	784	5	4.1	257	1	YGIE_ECOLI	P24198 escherichia
712	5	4.1	239	1	YOCB_HAEIN	P44197 haemophilus	785	5	4.1	258	1	C4BB_RAT	Q63515 rattus norv
713	5	4.1	240	1	CHV1_RHIME	P50350 rhizobium m	786	5	4.1	258	1	TEXF_RHLT	P42728 rhizobium 1
714	5	4.1	240	1	COLJ_ONCMF	Q04618 oncorhynch	787	5	4.1	258	1	YAAA_ECOLI	P11288 escherichia
715	5	4.1	240	1	KTHY_ASFB7	P42490 african swi	788	5	4.1	259	1	DEOC_ECOLI	P00882 escherichia
716	5	4.1	240	1	US19_HCMVA	P09725 human cytom	789	5	4.1	259	1	Y224_METJA	Q60283 methanococc
717	5	4.1	241	1	CTR3_YEAST	Q06686 saccharomyc	790	5	4.1	260	1	NQRC_PASMU	O9cl99 pasteurella
718	5	4.1	241	1	DCOP_THETH	P96076 thermus aqu	791	5	4.1	261	1	RFA4_HUMAN	Q13156 homo sapien
719	5	4.1	241	1	PSNA_SULSO	O9uxc6 sulfolobus	792	5	4.1	261	1	RNG7_MOUSE	P35737 mus musculu
720	5	4.1	241	1	TRUA_AQUAE	O68953 aquifex aeo	793	5	4.1	261	1	TAM_MYCTU	O53698 mycobacteri
721	5	4.1	241	1	Y26A_HAEIN	O86224 haemophilus	794	5	4.1	262	1	ATF6_ALLAR	P50363 allomyces a
722	5	4.1	242	1	HAP5_YEAST	Q02516 saccharomyc	795	5	4.1	262	1	ATP6_ALLMA	P50364 allomyces m
723	5	4.1	242	1	Y22T_AGRVI	Q34299 agrobacteri	796	5	4.1	262	1	GDAL_WHEAT	P04721 triticum ae
724	5	4.1	243	1	VLPE_MYCHR	O49537 mycoplasma	797	5	4.1	262	1	T2M1_MORSP	P11405 moraxella s
725	5	4.1	243	1	YH57_YEAST	P38833 saccharomyc	798	5	4.1	262	1	ZNUB_BUCAI	P57402 buchnera ap
726	5	4.1	244	1	COBI_PSEDE	P21639 pseudomonas	799	5	4.1	263	1	GP3D_CHLTR	P10557 chlamydia t
727	5	4.1	244	1	LPRA_MYCTU	Q11049 mycobacteri	800	5	4.1	263	1	SUMT_SYNY3	O55749 synechocyst
728	5	4.1	244	1	NQRC_HAEIN	P43957 haemophilus	801	5	4.1	264	1	GP3D_CHLMO	Q46439 chlamydia m
729	5	4.1	244	1	OSL3_ARATH	P50700 arabidopsis	802	5	4.1	264	1	HISA_SCHPO	Q10184 schizosacch
730	5	4.1	244	1	T2FC_YEAST	P35189 saccharomyc	803	5	4.1	264	1	YBAP_ECOLI	P77301 escherichia
731	5	4.1	245	1	143F_HUMAN	Q04917 homo sapien	804	5	4.1	265	1	COX3_AEGCO	Q36952 aegilops co
732	5	4.1	245	1	143F_MOUSE	P11576 mus musculu	805	5	4.1	265	1	COX3_HELAN	P32808 helianthus
733	5	4.1	245	1	PSA2_SCHPO	O94579 schizosacch	806	5	4.1	265	1	COX3_MAIZE	P09138 zea mays (m
734	5	4.1	245	1	SRA5_CAEEL	Q09207 caenorhabd1	807	5	4.1	265	1	COX3_OENBE	P08745 oenothera b
735	5	4.1	245	1	UL51_HSVEB	P28961 equine herp	808	5	4.1	265	1	COX3_ORYSA	P14852 oryza sativ
736	5	4.1	245	1	YABS_BACSU	P37561 bacillus su	809	5	4.1	265	1	COX3_SOYBN	P14853 glycine max
737	5	4.1	245	1	YH77_ARCFU	O28497 archaeoglob	810	5	4.1	265	1	COX3_VICFA	Q03227 vicia faba
738	5	4.1	246	1	VAD1_DROME	O9v7d2 drosophila	811	5	4.1	265	1	MYO2_LYCES	P54927 lycopersico
739	5	4.1	246	1	VATD_MANSE	Q9u0s4 manduca sex	812	5	4.1	265	1	SYNP_RAT	P22831 rattus norv
740	5	4.1	247	1	C21U_HUMAN	Q9ufm2 homo sapien	813	5	4.1	265	1	YCD4_YEAST	P25369 saccharomyc
741	5	4.1	247	1	C561_XENLA	Q91577 xenopus lae	814	5	4.1	265	1	YPR5_ECOLI	P22394 escherichia
742	5	4.1	247	1	PMGY_MYCLE	P53531 mycobacteri	815	5	4.1	266	1	HMUV_YERPE	Q56993 yersinia pe
743	5	4.1	247	1	TONB_SERMA	P26185 serratia ma	816	5	4.1	266	1	TRPL_CVACA	Q9tlw8 cyanidium c
744	5	4.1	247	1	VATD_BOVIN	P39942 bos taurus	817	5	4.1	266	1	Y032_TREPA	O83075 treponema p
745	5	4.1	247	1	VATD_HUMAN	Q9y5k8 homo sapien	818	5	4.1	267	1	DCOP_PICST	P49434 pichia stip
746	5	4.1	247	1	VATD_MOUSE	P57746 mus musculu	819	5	4.1	267	1	DCOP_YEAST	P03962 saccharomyc
747	5	4.1	247	1	FUCK_RABIT	Q97755 oryctolagus	820	5	4.1	267	1	FBOL_GALME	Q26427 galliera me
748	5	4.1	249	1	YH77_ARCFU	P44780 haemophilus	821	5	4.1	267	1	VATD_CANAL	P87220 candida alb
749	5	4.1	249	1	HMX1_CHICK	P28361 gallus gall	822	5	4.1	267	1	VNST_SFVS	P12792 sandfly fev
750	5	4.1	249	1	PKS1_BACSU	P40802 bacillus su	823	5	4.1	267	1	Y89Q_AQUAE	O67039 aquifex aeo
751	5	4.1	249	1	PSB1_HUMAN	Q06323 h proteasom	824	5	4.1	268	1	EXOR_RHIME	O52926 rhizobium m
752	5	4.1	249	1	PSB1_MACFA	P58238 macaca fasc	825	5	4.1	268	1	THIM_ARCFU	Q28204 archaeoglob
753	5	4.1	249	1	PSB1_MOUSE	P97371 mus musculu	826	5	4.1	268	1	TRPA_PASMU	P57854 pasteurella
754	5	4.1	249	1	PSB1_RAT	Q63797 rattus norv	827	5	4.1	269	1	AGAR_ECOLI	P42902 escherichia
755	5	4.1	249	1	VAD2_DROME	Q9nef6 drosophila	828	5	4.1	269	1	RFAZ_SALTY	P26473 salmonella
756	5	4.1	249	1	YC23_CVACA	O19904 cyanidium c	829	5	4.1	269	1	VI03_VACCC	P20499 vaccinia vi
757	5	4.1	250	1	PSA4_SFIOL	P52427 spinacia ol	830	5	4.1	269	1	VI03_VACCV	P12923 vaccinia vi
758	5	4.1	250	1	QCR_CACST	Q45659 bacillus st	831	5	4.1	269	1	YH93_AQUAE	P33000 variola vir
759	5	4.1	250	1	Y028_RICPR	O05972 rickettsia	832	5	4.1	270	1	HIS7_ARATH	O67862 aquifex aeo
760	5	4.1	251	1	TATC_RICPR	Q9zcg6 rickettsia	833	5	4.1	270	1	ISPD_STRCO	P34047 arabidopsis
761	5	4.1	251	1	UPPS_ANASQ	Q9zej7 anabaena sp	834	5	4.1	270	1	RA25_SCHPO	Q910q8 streptomyce
762	5	4.1	252	1	GSC_HUMAN	P56915 homo sapien	835	5	4.1	270	1	RA25_SCHPO	P42657 schizosacch
763	5	4.1	253	1	CIOB_MOUSE	P14106 mus musculu	836	5	4.1	270	1	TRUA_ECOLI	P07649 escherichia

837	5	4.1	270	1	VMT1_DHV11	Q01479	dhori virus	910	5	4.1	291	1	SIX2_HUMAN	Q09pc8	homo sapien
838	5	4.1	271	1	YE53_AQUAE	O67438	aquifex aeo	911	5	4.1	291	1	T2EB_HUMAN	P14984	homo sapien
839	5	4.1	271	1	ECE1_CANAL	Q07730	candida alb	912	5	4.1	292	1	NIFM_AZOVI	P14980	azotobacter
840	5	4.1	271	1	MT04_STRGO	Q9f305	streptomyce	913	5	4.1	292	1	Y761_TREPA	O83742	treponema p
841	5	4.1	271	1	YM35_MYCTU	Q10517	mycobacteri	914	5	4.1	293	1	CDSA_SVNY3	P73448	s phosphati
842	5	4.1	272	1	LYS5_YEAST	P50113	saccharomyc	915	5	4.1	293	1	COAT_PVSP	P16653	potato viru
843	5	4.1	273	1	TRY6_ANOGA	P35040	anopheles g	916	5	4.1	293	1	GLPO_BACSU	P37965	bacillus su
844	5	4.1	273	1	TRO_COTJA	Q08410	coturnix co	917	5	4.1	293	1	NIFH_AZOB	P17303	azospirillu
845	5	4.1	274	1	BAG1_HUMAN	Q99933	homo sapien	918	5	4.1	293	1	NIFM_AZOH	P23119	azotobacter
846	5	4.1	274	1	RS2_AQUAE	O67055	aquifex aeo	919	5	4.1	294	1	NIFM_ANASL	P33178	anabaena sp
847	5	4.1	274	1	PNK_AQUAE	O67809	aquifex aeo	920	5	4.1	294	1	NIFH_BRAJA	P06117	bradyrhizob
848	5	4.1	275	1	DHPS_HAEIN	P43776	haemophilus	921	5	4.1	294	1	NIFH_BRASP	P00463	mycorrhizob
849	5	4.1	275	1	NUEL_RHIME	P58909	rhizobium m	922	5	4.1	294	1	Y237_MYCPN	P75455	mycoplasma
850	5	4.1	275	1	ULL1_HCMVA	P16721	human cytom	923	5	4.1	294	1	YOGI_BACSU	P46340	bacillus su
851	5	4.1	275	1	UL34_HSVB	P28954	equine herp	924	5	4.1	295	1	ISPA_HAEIN	P45204	haemophilus
852	5	4.1	276	1	BACH_HALHP	Q48315	halobacteri	925	5	4.1	295	1	NIFL_RHOA	P08718	rhodospiril
853	5	4.1	276	1	BACH_HALHS	Q48314	halobacteri	926	5	4.1	295	1	NIFH_RHORU	P22921	rhodospiril
854	5	4.1	276	1	BACH_HALVA	P94853	haloarcula	927	5	4.1	296	1	CC2_DICDI	P34112	dictyostelli
855	5	4.1	276	1	COX2_HUMAN	O9v6n1	homo sapien	928	5	4.1	296	1	FTSX_BACSU	O34876	bacillus su
856	5	4.1	276	1	PANC_HELPY	P58061	helicobacte	929	5	4.1	296	1	NIFL_AZOCA	P26751	azorhizobiu
857	5	4.1	277	1	GFTI_HAPXE	O42154	haplochromi	930	5	4.1	296	1	NIF2_AZOCA	P26252	azorhizobiu
858	5	4.1	277	1	TRPC_PSEPU	P20578	pseudomonas	931	5	4.1	296	1	NIFH_PLEBO	Q00240	plectonema
859	5	4.1	278	1	PHZC_PSECL	Q51520	pseudomonas	932	5	4.1	296	1	NIFH_RHISN	P19068	rhizobium s
860	5	4.1	278	1	PHZF_PSEFL	Q51792	pseudomonas	933	5	4.1	296	1	PSTA_ECOLI	P07554	escherichia
861	5	4.1	278	1	TPPA_HUMAN	P49638	homo sapien	934	5	4.1	296	1	SIX2_MOUSE	Q62232	mus musculus
862	5	4.1	278	1	TPPA_RAT	P41034	rattus norv	935	5	4.1	297	1	NIFH_RHIE	P00461	rhizobium e
863	5	4.1	278	1	VG48_HSV11	Q00112	ictaluriid h	936	5	4.1	297	1	NIFH_RHIE	P00461	rhizobium e
864	5	4.1	279	1	LPXA_BRUB	P54080	brucella ab	937	5	4.1	297	1	NIFH_RHIME	P00460	rhizobium m
865	5	4.1	280	1	MDCB_PSEPU	Q92452	pseudomonas	938	5	4.1	297	1	VGIG_HRSV4	P27023	human respi
866	5	4.1	280	1	MURC_SYNP7	P95836	synecococc	939	5	4.1	297	1	VGIG_HRSV6	P27025	human respi
867	5	4.1	280	1	Y747_RICPR	Q92c13	rickettsia	940	5	4.1	297	1	VGIG_HRSV7	P27026	human respi
868	5	4.1	281	1	PSTA_METJA	Q58419	methanococc	941	5	4.1	298	1	RNH3_CHLPN	Q926j1	chlamydia p
869	5	4.1	281	1	YMF1_BACSU	P39648	bacillus su	942	5	4.1	298	1	VGIG_HRSV5	P27024	human respi
870	5	4.1	282	1	OPAB_BACSU	P46921	bacillus su	943	5	4.1	299	1	CRX_HUMAN	Q43186	homo sapien
871	5	4.1	282	1	PSTA_HAEIN	P45190	haemophilus	944	5	4.1	299	1	CRX_MOUSE	O54751	mus musculus
872	5	4.1	282	1	SRG2_CAEEL	P46571	caenorhabdi	945	5	4.1	299	1	HEM6_ECOLI	Q92874	homo sapien
873	5	4.1	282	1	VV_TPMV	Q9gm81	tupaia para	946	5	4.1	299	1	HEM6_ECOLI	P36553	escherichia
874	5	4.1	282	1	Y553_METJA	Q58650	methanococc	947	5	4.1	299	1	HEM6_SALTY	P33771	salmonella
875	5	4.1	283	1	EXXK_ADE02	P03242	human adeno	948	5	4.1	299	1	NIFH_ANASP	P00457	anabaena sp
876	5	4.1	283	1	INSK_ECOLI	P19769	escherichia	949	5	4.1	299	1	RL5_BOMMO	O76190	bombyx mori
877	5	4.1	283	1	LECH_MOUSE	P34927	mus musculus	950	5	4.1	299	1	YHJC_ECOLI	P37641	escherichia
878	5	4.1	283	1	LECH_RAT	P02706	rattus norv	951	5	4.1	300	1	RP32_AGRU	P50507	agrobacteri
879	5	4.1	283	1	T2AL_RUEGE	Q9khv6	ruegeria ge	952	5	4.1	302	1	MCRI_YEAST	P36060	saccharomyc
880	5	4.1	283	1	V585_BPBO3	Q37889	bacterioph	953	5	4.1	302	1	YBEJ_ECOLI	P37902	escherichia
881	5	4.1	284	1	NIF1_METTL	P25767	methanococc	954	5	4.1	302	1	YET6_YEAST	P40065	saccharomyc
882	5	4.1	284	1	YAGM_ECOLI	P71296	escherichia	955	5	4.1	304	1	ERA_BACHO	Q9k452	bacillus ha
883	5	4.1	285	1	LAFT_VIBPA	Q03477	vibrio para	956	5	4.1	304	1	Y687_HAEIN	P71356	haemophilus
884	5	4.1	285	1	PARP_ECOLI	P19071	escherichia	957	5	4.1	305	1	PYRB_SERMA	P19310	serratia ma
885	5	4.1	285	1	Y539_AQUAE	O6818	aquifex aeo	958	5	4.1	305	1	YYAM_BACSU	P37511	bacillus su
886	5	4.1	286	1	GDAO_WHEAT	P02863	tritium ae	959	5	4.1	306	1	CH38_DROME	P07183	drosophila
887	5	4.1	286	1	MEPA_HAEIN	P44566	haemophilus	960	5	4.1	306	1	YL86_CAEEL	P34444	caenorhabdi
888	5	4.1	286	1	RT28_YEAST	P21771	saccharomyc	961	5	4.1	306	1	YQXF_BACSU	P54569	bacillus su
889	5	4.1	286	1	YGBB_EDWTC	O52401	edwardsiell	962	5	4.1	307	1	CIW8_MOUSE	Q922t1	mus musculus
890	5	4.1	286	1	YNIA_ECO57	P58065	escherichia	963	5	4.1	307	1	PYRB_HELPJ	Q92m81	helicobacte
891	5	4.1	286	1	YNIA_ECOLI	P77739	escherichia	964	5	4.1	307	1	PYRB_HELPY	O25716	helicobacte
892	5	4.1	287	1	NIFH_FRAAL	P08925	frankia aln	965	5	4.1	307	1	RNHL_YEAST	P53942	saccharomyc
893	5	4.1	287	1	PPCK_SALTY	P41033	salmonella	966	5	4.1	308	1	FTSQ_BARBA	Q9x5h9	bartonella
894	5	4.1	287	1	YJWJ_ECOLI	P39409	escherichia	967	5	4.1	308	1	Y311_METJA	Q58437	methanococc
895	5	4.1	288	1	BLC3_PSEAE	P37322	pseudomonas	968	5	4.1	309	1	FSTL_FLABI	P52838	flaveria bi
896	5	4.1	288	1	BLC6_VIBCH	P81781	vibrio chol	969	5	4.1	309	1	IK11_YEAST	P38874	saccharomyc
897	5	4.1	288	1	BLP1_PSEAE	Q03170	pseudomonas	970	5	4.1	309	1	PYRB_VIBS2	P96174	vibrio sp.
898	5	4.1	288	1	HME2_CHICK	P16897	pseudomonas	971	5	4.1	310	1	DOS1_YEAST	P54858	saccharomyc
899	5	4.1	289	1	KPPR_ECOLI	Q05917	gallus gall	972	5	4.1	310	1	LACC_STAAT	P11099	staphylococ
900	5	4.1	289	1	KPPR_ECOLI	P37307	escherichia	973	5	4.1	311	1	DO34_YEAST	P33309	saccharomyc
901	5	4.1	289	1	MTW1_YEAST	P39731	saccharomyc	974	5	4.1	311	1	V311_ASEB7	P23163	african swi
902	5	4.1	289	1	RIPS_TRIKI	P24478	trichosan	975	5	4.1	311	1	YXAF_BACSU	Q07835	bacillus su
903	5	4.1	289	1	V510_ARCFU	O25740	archaeoglob	976	5	4.1	312	1	CAH4_BOVIN	Q95323	bos taurin
904	5	4.1	290	1	LECH_HUMAN	P07306	homo sapien	977	5	4.1	312	1	CAH4_HUMAN	P22748	homo sapien
905	5	4.1	290	1	T2M3_METJA	Q58017	methanococc	978	5	4.1	312	1	COAA_VIBCH	Q9kv38	vibrio chol
906	5	4.1	291	1	BACH_NATPH	P15647	natronomona	979	5	4.1	313	1	CIW6_HUMAN	Q9v257	homo sapien
907	5	4.1	291	1	ISPA_MICLU	O66126	micrococc	980	5	4.1	313	1	GD47_WHEAT	P04727	tritium ae
908	5	4.1	291	1	KPPR_ALCEU	P19924	alcaligenes	981	5	4.1	313	1	M2OM_RAT	P97700	rattus norv
909	5	4.1	291	1	KPPR_ALCEU	P19923	alcaligenes	982	5	4.1	313	1	SPBB_STRCL	P37819	streptomyce

983 5 4.1 313 1 TFS2_DROME
 984 5 4.1 313 1 YDCU_ECOLI
 985 5 4.1 314 1 CYF_ODOSI
 986 5 4.1 314 1 TPIC_FRAAN
 987 5 4.1 314 1 YHML_YEAST
 988 5 4.1 315 1 SOL2_YEAST
 989 5 4.1 315 1 VN32_HUMAN
 990 5 4.1 315 1 VN32_ROTTL
 991 5 4.1 316 1 KHSE_MYCTU
 992 5 4.1 317 1 TPB3_HALNL
 993 5 4.1 317 1 YG98_MYCLE
 994 5 4.1 318 1 NIA_CHLVU
 995 5 4.1 318 1 NUIM_BALMU
 996 5 4.1 318 1 NUIM_BOVIN
 997 5 4.1 318 1 NUIM_PIG
 998 5 4.1 319 1 AES_ECOLI
 999 5 4.1 319 1 GCP_MYCPN
 1000 5 4.1 319 1 GDA5_WHEAT

ALIGNMENTS

RESULT 1
 ID TKNK_MOUSE STANDARD; PRT; 116 AA.
 AC P55099;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE NEUROKININ B PRECURSOR (NEUROMEDIN K) (PREPROTACHYKININ B) (PPT-B).
 GN TAC3 OR NKNB OR TAC2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=1090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;
 RA Koko K., Muneoka E., Hosaka M., Murakami K., Nakayama K.;
 RT "Cloning and sequence analysis of mouse cDNAs encoding
 preprotachykinin A and B."
 RL Biomed. Res. 14:253-259(1993).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 MUSCLES.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
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 CC -----
 CC EMBL: D14423; BAA03316.1; ..
 CC MGD: MGI:98476; Tac2.
 DR InterPro: IPR003635; Neurokinin.
 DR InterPro: IPR002040; Tachykinin.
 DR ProDom: PD020370; Neurokinin; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 KW Amidation; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT PEPTIDE 82 91 NEUROKININ B.
 FT MOD_RES 91 91 AMIDATION (G-92 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 116 AA; 12809 MW; BF6E89373E2031CC CRG64;

Query Match 8.3%; Score 10; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.0028;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 79 KRDHDFVVG 88
 DB 80 KRDHDFVVG 89
 RESULT 2
 ID TKNK_RAT STANDARD; PRT; 116 AA.
 AC P08435;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE NEUROKININ B PRECURSOR (NEUROMEDIN K).
 GN TAC3 OR NKNB OR NKB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=88051833; PubMed=3479225;
 RA Bonner T.I., Aifolter H.-U., Young A.C., Young W.S. III;
 RT "A cDNA encoding the precursor of the rat neuropeptide, neurokinin
 B."
 RL Brain Res. 388:243-249(1987).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 MUSCLES.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
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 CC -----
 CC EMBL: M16410; AAA41711.1; ..
 CC PIR: A43779; A43779.
 DR InterPro: IPR003635; Neurokinin.
 DR InterPro: IPR002040; Tachykinin.
 DR ProDom: PD020370; Neurokinin; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 KW Amidation; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT PEPTIDE 82 91 NEUROKININ B.
 FT MOD_RES 91 91 AMIDATION (G-92 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 116 AA; 12659 MW; C73EC67F2BAF8C8C CRG64;
 Query Match 8.3%; Score 10; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 79 KRDHDFVVG 88
 DB 80 KRDHDFVVG 89
 RESULT 3
 ID TKNK_BOVIN STANDARD; PRT; 126 AA.
 AC P08856;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE NEUROKININ B PRECURSOR (NEUROMEDIN K).
 GN TAC3 OR NKNB OR NKB.

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86313713; PubMed=3462746;
RA Kotani H., Hoshimaru M., Nawa H., Nakanishi S.;
RT "Structure and gene organization of bovine neuromedin K precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:7074-7078(1986).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M14351; AAA30723.1; JOINED.
DR EMBL; M14347; AAA30723.1; JOINED.
DR EMBL; M14348; AAA30723.1; JOINED.
DR EMBL; M14349; AAA30723.1; JOINED.
DR EMBL; M14350; AAA30723.1; JOINED.
DR PIR; A25905; A25905.
DR InterPro; IPR003635; Neurokinin.
DR InterPro; IPR002040; Tachykinin.
DR ProDom; PD020370; Neurokinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PEPTIDE 86 95 NEUROKININ B.
FT MOD_RES 95 95 AMIDATION (G-96 PROVIDE AMIDE GROUP).
SQ SEQUENCE 126 AA; 13871 MW; 446EF433498EC059 CRC64;

Query Match 8.3%; Score 10; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 KRDMHDFVVG 88
DB 84 KRDMHDFVVG 93
|||||
[1]
RESULT 4
ID TNKK_PIG STANDARD; PRT; 10 AA.
AC P01292;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NEUROKININ B (NEUROMEDIN K).
GN TAC3 OR NKNB OR NKB.
OS Sus scrofa (Pig), and Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823, 8406;
[1]
RP SEQUENCE.
RC SPECIES-Pig; TISSUE-Spinal cord;
RX MEDLINE=83282812; PubMed=6576785;
RA Kangawa K., Minamino N., Fukuda A., Matsuo H.;
RT "Neuromedin K: a novel mammalian tachykinin identified in porcine
RT spinal cord."
RL Biochem. Biophys. Res. Commun. 114:533-540(1983).

RP SEQUENCE.
RC SPECIES-R. ridibunda; TISSUE-Brain;
RX MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog Rana ridibunda.";
RL J. Neurochem. 57:2086-2091(1991).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC
CC PIR; A01560; SPPGNK.
DR InterPro; IPR002040; Tachykinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1211 MW; E1FA7C62C9C9CAAL CRC64;

Query Match 6.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 DMHDFVVG 88
DB 1 DMHDFVVG 8
|||||
[1]
RESULT 5
ID POLG_PEMVM STANDARD; PRT; 3099 AA.
AC O56075;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);
DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
DE (EC 3.4.22.44) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
DE COAT PROTEIN (CP)].
OS Peanut mottle virus (strain M).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=103926;
[1]
RP SEQUENCE FROM N.A.
RA Flasinski S., Gonzales R.A., Cassidy B.G.;
RT "The complete nucleotide sequence of peanut mottle virus (M strain)
RT genomic RNA.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHD
CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -!- CATALYTIC ACTIVITY: NUCLEAR INCLUSION PROTEIN A HYDROLYSES
CC GLUTAMINYL BONDS, AND ACTIVITY IS FURTHER RESTRICTED BY
CC PREFERENCES FOR THE AMINO ACIDS IN P6-P1 THAT VARY WITH THE
CC SPECIES OF POTYVIRUS, E.G. GLU-XAA-TYR-XAA-GLN+(SER OR GLY)
CC FOR THE ENZYME FROM TOBACCO ETCH VIRUS. THE NATURAL SUBSTRATE IS
CC THE VIRAL POLYPROTEIN, BUT OTHER PROTEINS AND OLIGOPETIDES
CC CONTAINING THE APPROPRIATE CONSENSUS SEQUENCE ARE ALSO CLEAVED.
CC -!- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -!- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.

CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
CC -----
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CC -----
DR EMBL: AF023848; BAB94595.1; -
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR001730; Peptidase_C4.
DR InterPro: IPR001456; Peptidase_C6.
DR InterPro: IPR002540; Poly_P1.
DR InterPro: IPR001592; Poly_coat.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00270; DEAD; 1.
DR Pfam: PF00863; Peptidase_C4; 1.
DR Pfam: PF00851; Peptidase_C6; 1.
DR Pfam: PF00767; Poly_coat; 1.
DR Pfam: PF01577; Poly_P1; 1.
DR Pfam: PF00880; RNA_dep_RNA_pol; 1.
DR PRINTS: PR00966; NIAPOTYPASE.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
KW ATP-binding.
FT CHAIN 1 322 N-TERMINAL PROTEIN.
FT CHAIN 323 779 HELPER COMPONENT PROTEINASE.
FT CHAIN 780 1128 PROTEIN P3.
FT CHAIN 1129 1180 6 KDA PROTEIN 1.
FT CHAIN 1181 1814 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1815 1867 6 KDA PROTEIN 2.
FT CHAIN 1868 ? GENOME-LINKED PROTEIN.
FT CHAIN 7 2303 NUCLEAR INCLUSION PROTEIN A.
FT CHAIN 2304 2821 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 2822 3099 COAT PROTEIN.
FT CHAIN 1868 2303 PUTATIVE NUCLEAR INCLUSION PROTEIN A.
FT NP_BIND 1285 1272 ATP (POTENTIAL).
SQ SEQUENCE 3099 AA; 351032 MW; 0D8E9FC7603F0A4B CRC64;

Query Match 6.6%; Score 8; DB 1; Length 3099;
Best Local Similarity 100.0%; Pred.No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 EEVYVGGG 35
Db 546 EEVYVGGG 553
|||||||
STANDARD; PRT; 310 AA.

RESULT 6
YN00_MYCTU
ID YN00_MYCTU STANDARD; PRT; 310 AA.
AC Q50655;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 34.4 KDA PROTEIN RV2300C.
GN RV2300C OR MT2357 OR MTCY339.09.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sultón J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL: Z77163; CAB00971.1; -
DR EMBL: AE007078; AAK46642.1; -
DR TIGR: MT2357; -
DR Tuberculist: RV2300C; -
DR InterPro: IPR001279; Beta_lactam_met.
DR Pfam: PF00753; lactamase_B; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 310 AA; 34352 MW; 0764F4FA64AB5E51 CRC64;

Query Match 5.8%; Score 7; DB 1; Length 310;
Best Local Similarity 100.0%; Pred.No. 9.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 DPDLYQL 46
Db 299 DPDLYQL 305
|||||||
STANDARD; PRT; 590 AA.

RESULT 7
GRK5_BOVIN
ID GRK5_BOVIN STANDARD; PRT; 590 AA.
AC P43249;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR KINASE GRK5 (EC 2.7.1.-).
GN GPRK5 OR GRK5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tongue epithelium;
RX MEDLINE=94165084; PubMed=8120045;
RA Fremont R.T., Koch W.J., Inglesse J., Lefkowitz R.J.;
RT "Identification, purification, and characterization of GRK5, a member
RT of the family of G protein-coupled receptor kinases.";
RL J. Biol. Chem. 269:6832-6841(1994).
CC -1- FUNCTION: SPECIFICALLY PHOSPHORYLATES THE ACTIVATED FORMS OF G
CC PROTEIN-COUPLED RECEPTORS.

CC -!- TISSUE SPECIFICITY: HIGHEST LEVELS IN LUNG, HEART, RETINA, LINGUAL
CC EPIPHELIUM. VERY LITTLE IN BRAIN, LIVER, KIDNEY.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC GPRK SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC
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CC
CC EMBL; U01206; AAA17561.1;
CC HSSP; Q63450; IA06.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR000239; GPCR_kinase.
CC InterPro: IPR000961; Pkinase_C.
CC InterPro: IPR000342; RGS.
CC InterPro: IPR002290; Ser_thr_kin_actsite.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00615; RGS; 1.
CC PRINTS; PR00717; GPCR_KINASE.
CC SMART; SM00315; RGS; 1.
CC SMART; SM00133; S_TK_X; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS0132; RGS; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 1 185 N-TERMINAL.
FT DOMAIN 186 448 PROTEIN KINASE.
FT DOMAIN 449 590 C-TERMINAL.
FT NP_BIND 192 200 ATP (BY SIMILARITY).
FT BINDING 215 215 ATP (BY SIMILARITY).
FT ACT_SITE 311 311 BY SIMILARITY.
FT MOD_RES 484 484 PHOSPHORYLATION (AUTO-).
FT MOD_RES 485 485 PHOSPHORYLATION (AUTO-).
SQ SEQUENCE 590 AA; 67888 MW; E8F353697D8BA6E2 CRC64;

Query Match 5.8%; Score 7; DB 1; Length 590;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LLQRLFK 52
DB 550 LLQRLFK 556

RESULT 8
GRK5_HUMAN
ID GRK5_HUMAN STANDARD; PRT; 590 AA.
AC P34947;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR KINASE GRK5 (EC 2.7.1.-).
GN GRK5 OR GRK5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93296183; PubMed=7685906;
RA Kunapuli P., Benovic J.L.;
RT "Cloning and expression of GRK5: a member of the G protein-coupled
RT receptor kinase family."

RL Proc. Natl. Acad. Sci. U.S.A. 90:5588-5592(1993).
CC -!- FUNCTION: SPECIFICALLY PHOSPHORYLATES THE ACTIVATED FORMS OF G
CC PROTEIN-COUPLED RECEPTORS.
CC -!- TISSUE SPECIFICITY: HIGHEST LEVELS IN HEART, PLACENTA, LUNG >
CC SKELETAL MUSCLE > BRAIN, LIVER, PANCREAS > KIDNEY.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC GPRK SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC
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CC
CC EMBL; L15388; AAA58620.1;
CC HSSP; Q63450; IA06.
CC MIM; 600870;
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR000239; GPCR_kinase.
CC InterPro: IPR000961; Pkinase_C.
CC InterPro: IPR000342; RGS.
CC InterPro: IPR002290; Ser_thr_kin_actsite.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00615; RGS; 1.
CC PRINTS; PR00717; GPCR_KINASE.
CC SMART; SM00315; RGS; 1.
CC SMART; SM00220; S_TK_X; 1.
CC SMART; SM00133; S_TK_X; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
CC PROSITE; PS0132; RGS; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 1 185 N-TERMINAL.
FT DOMAIN 186 448 PROTEIN KINASE.
FT DOMAIN 449 590 C-TERMINAL.
FT NP_BIND 192 200 ATP (BY SIMILARITY).
FT BINDING 215 215 ATP (BY SIMILARITY).
FT ACT_SITE 311 311 BY SIMILARITY.
FT MOD_RES 484 484 PHOSPHORYLATION (AUTO-).
FT MOD_RES 485 485 PHOSPHORYLATION (AUTO-).
SQ SEQUENCE 590 AA; 67786 MW; D363567ECFF5CF21 CRC64;

Query Match 5.8%; Score 7; DB 1; Length 590;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LLQRLFK 52
DB 550 LLQRLFK 556

RESULT 9
CCMF_HAEIN
ID CCMF_HAEIN STANDARD; PRT; 648 AA.
AC P45037;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCMF.
GN CCMF OR H1094.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.

```
RC STRAIN-RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Felschmann R.D., Bult C.J., Tomb J.-F., Dougherty B.A., Kirkness E.F.,
RA Kerlavage A.R., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA McKenney K., Shirey R., Liu L.-I., Glodek A., Kelley J.M.,
RA Scott J.D., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: REQUIRED FOR THE BIOGENESIS OF C-TYPE CYTOCHROMES.
CC -!- POSSIBLE SUBUNIT OF A HEME LIASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCLI/NRFE/CCSA FAMILY.
CC -----
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CC -----
CC EMBL: U32789; AAC22751.1; -.
CC TIGR: H11094; -.
CC InterPro: IPR002541; CytC_asm.
CC InterPro: IPR003567; CytC_blog.
CC Pfam: PF01578; CytC_asm; 1.
CC Cytochrome c-type biogenesis; Transmembrane; Inner membrane;
KW Complete proteome.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 43 63 POTENTIAL.
FT TRANSMEM 94 114 POTENTIAL.
FT TRANSMEM 122 142 POTENTIAL.
FT TRANSMEM 176 196 POTENTIAL.
FT TRANSMEM 211 231 POTENTIAL.
FT TRANSMEM 274 294 POTENTIAL.
FT TRANSMEM 312 332 POTENTIAL.
FT TRANSMEM 352 372 POTENTIAL.
FT TRANSMEM 394 414 POTENTIAL.
FT TRANSMEM 424 444 POTENTIAL.
FT TRANSMEM 448 468 POTENTIAL.
FT TRANSMEM 490 510 POTENTIAL.
FT TRANSMEM 616 636 POTENTIAL.
SQ SEQUENCE 648 AA; 72353 MW; ABE434B80F4B92B6 CRC64;

Query Match 5.8%; Score 7; DB 1; Length 648;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AILAFSL 15
Db 280 AILAFSL 286
|||||||

RESULT 10
ATX1_MOUSE
ID ATX1_MOUSE STANDARD; PRT; 792 AA.
AC P54254;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ATAXIN-1 (SPINOCEREBELLAR ATAXIA TYPE 1 PROTEIN).
GN SCAL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Brain, Thymus, and Retina;
RX MEDLINE=95381424; PubMed=8789437;
RA Banfi S., Servadio A., Chung M.-Y., Capozzoli F., Duvick L.A.,
RA Elde R., Zoghbi H.Y., Orr H.T.;
RT "Cloning and developmental expression analysis of the murine homolog
RT of the spinocerebellar ataxia type 1 gene (Scal).";
RL Hum. Mol. Genet. 5:33-40(1996).
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. IN BRAIN, THE PATTERN OF
CC DISTRIBUTION IS LIMITED TO NEURONS POPULATIONS.
CC -!- DEVELOPMENTAL STAGE: TRANSIENT EXPRESSION BURST IN PURKINJE CELLS
CC AS THE CEREBELLAR CORTEX BECOMES FUNCTIONAL (POSTNATAL DAY 14),
CC AND IN MESENCHYMAL CELLS OF THE DEVELOPING INTERVERTEBRAL DISCS OF
CC THE SPINAL COLUMN.
CC -!- POLYMORPHISM: THE MURINE POLY-GLN REGION IS VERY LIMITED IN
CC COMPARISON TO THE HUMAN SCAL AND IS NOT POLYMORPHIC.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X83542; CAA58533.1; -.
CC HSP: Q12967; 2RGF.
CC MGD; MGI:104783; Scal.
CC InterPro: IPR003652; Atax_HMG.
CC SMART; SM00536; AXH; 1.
CC DOMAIN 214 217 POLY-PRO.
CC SEQUENCE 792 AA; 84052 MW; CA5F59C0013499DB CRC64;

Query Match 5.8%; Score 7; DB 1; Length 792;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 GLLKALS 65
Db 75 GLLKALS 81
|||||||

RESULT 11
HIG2_HUMAN
ID HIG2_HUMAN STANDARD; PRT; 63 AA.
AC Q9YSL2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOXIA-INDUCIBLE PROTEIN 2.
GN HIG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=20155117; PubMed=10690527;
RA Denko N.C., Schindler C., Koong A., Laderoute K., Green C.,
RA Giaccia A.J.;
RT "Epigenetic regulation of gene expression in cervical cancer cells by
RT the tumor microenvironment.";
RL Clin. Cancer Res. 6:480-487(2000).
CC -----
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CC -----
DR EMBL; AF144755; AAD37585.1; -
KW TRANSMEMBRANE.
FT TRANSMEM 7 23 POTENTIAL.
SQ SEQUENCE 53 AA; 6950 MW; 91EA626A511FC8B7 CRC64;

Query Match 5.0%; Score 6; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 SLEGLL 61
|||||
DB 26 SLEGLL 31

RESULT 12
SAS2_BACME STANDARD; PRT; 73 AA.
AC P10571;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE SMALL, ACID-SOLUBLE SPORE PROTEIN C2 (SASP).
GN SASP-C2.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85286345; PubMed=3928443;
RA Fliss E.R., Setlow P.;
RT "Genes for Bacillus megaterium small, acid-soluble spore proteins: nucleotide sequence of two genes and their expression during sporulation."
RL Gene 35:151-157(1985).
CC -!- FUNCTION: SASP ARE BOUND TO SPORE DNA. THEY ARE DOUBLE-STRANDED DNA-BINDING PROTEINS THAT CAUSE DNA TO CHANGE TO AN A-LIKE CONFORMATION. THEY PROTECT THE DNA BACKBONE FROM CHEMICAL AND ENZYMIC CLEAVAGE AND ARE THUS INVOLVED IN DORMANT SPORE'S HIGH RESISTANCE TO UV LIGHT.
CC -!- MISCELLANEOUS: SASP ARE DEGRADED IN THE FIRST MINUTES OF SPORE GERMINATION AND PROVIDE AMINO ACIDS FOR BOTH NEW PROTEIN SYNTHESIS AND METABOLISM.
CC -!- SIMILARITY: BELONGS TO THE ALPHA/BETA-TYPE SASP FAMILY.

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CC EMBL; M10920; -; NOT_ANNOTATED_CDS.
DR PIR; B24033; B24033.
DR InterPro; IPR001448; SASP.
DR Pfam; PF00269; SASP; 1.
DR PROSITE; PS00304; SASP_1; 1.
DR PROSITE; PS00684; SASP_2; 1.
KW DNA-binding; Sporulation; Multigene family.
FT SITE 27 28 CLEAVAGE (BY SPORE PROTEASE).
SQ SEQUENCE 73 AA; 7731 MW; C44EFAFFCAFB24F CRC64;

Query Match 5.0%; Score 6; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GGGRSK 38

DB 65 GGGRSK 70
|||||

RESULT 13
SAS5_BACME STANDARD; PRT; 73 AA.
ID SAS5_BACME
AC P04835;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE SMALL, ACID-SOLUBLE SPORE PROTEIN C5 (SASP).
GN SASP-C5.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86111611; PubMed=3080406;
RA Fliss E.R., Loshon C.A., Setlow P.;
RT "Genes for Bacillus megaterium small, acid-soluble spore proteins: cloning and nucleotide sequence of three additional genes from this multigene family."
RL J. Bacteriol. 165:467-473(1986).
CC -!- FUNCTION: SASP ARE BOUND TO SPORE DNA. THEY ARE DOUBLE-STRANDED DNA-BINDING PROTEINS THAT CAUSE DNA TO CHANGE TO AN A-LIKE CONFORMATION. THEY PROTECT THE DNA BACKBONE FROM CHEMICAL AND ENZYMIC CLEAVAGE AND ARE THUS INVOLVED IN DORMANT SPORE'S HIGH RESISTANCE TO UV LIGHT.

CC -!- MISCELLANEOUS: SASP ARE DEGRADED IN THE FIRST MINUTES OF SPORE GERMINATION AND PROVIDE AMINO ACIDS FOR BOTH NEW PROTEIN SYNTHESIS AND METABOLISM.
CC -!- SIMILARITY: BELONGS TO THE ALPHA/BETA-TYPE SASP FAMILY.

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CC EMBL; M14111; AAA22284.1;
DR PIR; C24543; C24543.
DR InterPro; IPR001448; SASP.
DR Pfam; PF00269; SASP; 1.
DR PROSITE; PS00304; SASP_1; 1.
DR PROSITE; PS00684; SASP_2; 1.
KW DNA-binding; Sporulation; Multigene family.
FT SITE 27 28 CLEAVAGE (BY SPORE PROTEASE).
SQ SEQUENCE 73 AA; 7680 MW; 5B1455977DC3A025 CRC64;

Query Match 5.0%; Score 6; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GGGRSK 38
|||||

DB 65 GGGRSK 70
|||||

RESULT 14
Y084_TREPA STANDARD; PRT; 77 AA.
ID Y084_TREPA
AC O83122;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN TP0084.
GN TP0084.
OS Treponema pallidum.

OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=NICHOLS;

RX MEDLINE=98332770; PubMed=9665876;

RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,

RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,

RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,

RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,

RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,

RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,

RA Venter J.C.;

RT "Complete genome sequence of Treponema pallidum, the syphilis

RT Spirochete";

RL Science 281:375-388(1998).

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CC -----

DR EMBL; AE001193; AAC65088.1; -

DR TIGR; TP0084; -

DR InterPro: IPR000515; BPD_transp.

KW Hypothetical protein. Complete proteome.

SQ SEQUENCE 77 AA; 8224 MW; 09046A5D92463942 CRC64;

Query Match 5.0%; Score 6; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 ESTSPE 78

Db | | | | |

Db 32 ESTSPE 37

RESULT 15

YJB8_YEAST

ID YJB8_YEAST STANDARD; PRT; 104 AA.

AC P47070;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE HYPOTHETICAL 11.7 KDA PROTEIN IN PET130-CCT3 INTERGENIC REGION.

GN YJL018W OR J1315.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RA To Van D., Perea J., Jacq C.;

RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.

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CC -----

DR EMBL; Z49294; CA89310.1; -

DR SGD; S0003555; YJL018W.

KW Hypothetical protein.

SQ SEQUENCE 104 AA; 11675 MW; A0AA3D1E4C896ACA CRC64;

Query Match 5.0%; Score 6; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 NVPSEFG 112

Db | | | | |

Db 93 NVPSEFG 98

Search completed: May 3, 2002, 12:32:13
Job time: 204 sec

GenCore version 4.5
Copyright (c) 1993-2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2002, 12:28:33 ; Search time 22.27 Seconds
(without alignments)
794.744 Million cell updates/sec

Title: US-09-852-659-85
Perfect score: 121
Sequence: 1 MRIMLLFTALAFSLAQSGF.....DVNQENVPFGILKYPPRAE 121

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 473505 seqs, 146272329 residues

Word size : 0

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000.

Post-processing: Listing first 1000 summaries

Database :

SPTREMBL17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	54.5	121	4 Q9UHF0	Q9UHF0 homo sapien
2	10	8.3	116	11 Q9QXS9	Q9QXS9 mus musculus
3	8	6.6	812	2 Q9RT53	Q9RT53 deinococcus
4	7	5.8	50	8 Q9BVP5	Q9BVP5 lotus japon
5	7	5.8	98	8 Q9B2G1	Q9B2G1 isodon mac
6	7	5.8	143	2 P73929	P73929 synecocyst
7	7	5.8	286	5 Q9VFR0	Q9VFR0 drosophila
8	7	5.8	297	8 Q9VFR0	Q9VFR0 drosophila
9	7	5.8	348	9 Q9MCB7	Q9MCB7 lactococcus
10	7	5.8	348	9 Q9MCB8	Q9MCB8 lactococcus
11	7	5.8	350	9 Q9MCB8	Q9MCB8 lactococcus
12	7	5.8	366	8 Q9Z255	Q9Z255 neurospora
13	7	5.8	377	2 Q9PH30	Q9PH30 xylella fas
14	7	5.8	388	5 Q9RVF4	Q9RVF4 manduca sex
15	7	5.8	394	2 Q9NFC7	Q9NFC7 deinococcus
16	7	5.8	405	5 Q9NFC7	Q9NFC7 deinococcus
17	7	5.8	418	2 Q9CLM9	Q9CLM9 pasteurella
18	7	5.8	475	2 Q9PPC5	Q9PPC5 campylobact
19	7	5.8	480	9 Q38300	Q38300 lactococcus

20	7	5.8	481	9 Q38239	Q38239 bacterioph
21	7	5.8	483	10 Q9XEL2	Q9XEL2 brassica ju
22	7	5.8	493	10 P92947	P92947 arabidopsi
23	7	5.8	493	10 Q9CAK5	Q9CAK5 arabidopsi
24	7	5.8	496	2 Q9HWJ2	Q9HWJ2 pseudomon
25	7	5.8	533	2 Q9Z9N5	Q9Z9N5 bacillus ha
26	7	5.8	534	2 Q9KE54	Q9KE54 bacillus ha
27	7	5.8	608	5 Q9V6D4	Q9V6D4 drosophila
28	7	5.8	637	11 Q9CZ01	Q9CZ01 mus muscu
29	7	5.8	702	2 Q9CPW7	Q9CPW7 pasteurella
30	7	5.8	751	10 Q9FR11	Q9FR11 arabidopsi
31	7	5.8	712	5 Q76408	Q76408 caenorhabd
32	7	5.8	1015	11 Q9D4G5	Q9D4G5 mus muscu
33	7	5.8	1038	10 Q9LE41	Q9LE41 arabidopsi
34	7	5.8	1058	10 Q9LEZ5	Q9LEZ5 arabidopsi
35	7	5.8	1190	10 Q9FNB4	Q9FNB4 arabidopsi
36	7	5.8	1516	10 Q24525	Q24525 arabidopsi
37	7	5.8	3734	3 Q9C1G0	Q9C1G0 kallichroma
38	6	5.0	28	10 Q9S886	Q9S886 citrus sine
39	6	5.0	48	11 Q64224	Q64224 rattus norv
40	6	5.0	49	9 Q9T115	Q9T115 lactobacill
41	6	5.0	63	2 Q9F0S8	Q9F0S8 thermus aqu
42	6	5.0	76	10 Q9M687	Q9M687 gossypium r
43	6	5.0	79	5 Q26801	Q26801 trypanosoma
44	6	5.0	84	12 Q98873	Q98873 turkey herp
45	6	5.0	87	12 Q41132	Q41132 paramecium
46	6	5.0	92	12 Q38024	Q38024 potato viru
47	6	5.0	92	12 Q69331	Q69331 salmeline
48	6	5.0	93	4 Q9UMM4	Q9UMM4 homo sapien
49	6	5.0	93	4 Q9UMM3	Q9UMM3 homo sapien
50	6	5.0	93	4 Q9UMM2	Q9UMM2 homo sapien
51	6	5.0	97	5 Q22828	Q22828 caenorhabd
52	6	5.0	98	2 P96728	P96728 bacillus su
53	6	5.0	99	10 Q9SB36	Q9SB36 arabidopsi
54	6	5.0	99	10 Q02024	Q02024 lycopersico
55	6	5.0	99	12 Q9QML0	Q9QML0 human immu
56	6	5.0	100	8 Q9T6E7	Q9T6E7 felis silve
57	6	5.0	101	12 Q72611	Q72611 human immu
58	6	5.0	101	12 Q97062	Q97062 human immu
59	6	5.0	101	12 Q9QML8	Q9QML8 human immu
60	6	5.0	101	12 Q9Q616	Q9Q616 human immu
61	6	5.0	101	12 Q9Q610	Q9Q610 human immu
62	6	5.0	101	12 Q9DG06	Q9DG06 human immu
63	6	5.0	102	12 P88159	P88159 human immu
64	6	5.0	104	11 Q62802	Q62802 rattus norv
65	6	5.0	105	1 O58809	O58809 pyrococcus
66	6	5.0	105	2 Q9KR06	Q9KR06 vibrio chol
67	6	5.0	106	3 P79033	P79033 emerice
68	6	5.0	108	11 Q9CVC4	Q9CVC4 mus muscu
69	6	5.0	108	12 Q9QNN0	Q9QNN0 potato viru
70	6	5.0	109	5 Q18399	Q18399 caenorhabd
71	6	5.0	111	4 Q9UI65	Q9UI65 homo sapien
72	6	5.0	111	4 Q9H4W3	Q9H4W3 homo sapien
73	6	5.0	111	11 Q99JK5	Q99JK5 mus muscu
74	6	5.0	117	2 Q9JN12	Q9JN12 agrobacteri
75	6	5.0	120	10 Q02022	Q02022 lycopersico
76	6	5.0	127	5 Q02000	Q02000 chrysaora g
77	6	5.0	128	3 Q93805	Q93805 tricholoma
78	6	5.0	131	11 Q9D2T1	Q9D2T1 mus muscu
79	6	5.0	132	10 Q02021	Q02021 lycopersico
80	6	5.0	133	2 Q9KH64	Q9KH64 uncultured
81	6	5.0	134	2 Q9K3B2	Q9K3B2 uncultured
82	6	5.0	134	2 Q9KJE2	Q9KJE2 lactococcus
83	6	5.0	134	5 P90530	P90530 dictyosteli
84	6	5.0	134	8 Q9G379	Q9G379 felis silve
85	6	5.0	143	9 Q03904	Q03904 bacterioph
86	6	5.0	145	2 Q9RK57	Q9RK57 streptomyc
87	6	5.0	152	1 Q9YAN1	Q9YAN1 aeropyrum p
88	6	5.0	153	1 Q9Y8X9	Q9Y8X9 aeropyrum p
89	6	5.0	156	4 Q14924	Q14924 homo sapien
90	6	5.0	156	11 Q9CQ49	Q9CQ49 mus muscu
91	6	5.0	157	2 Q99YT5	Q99YT5 streptococ
92	6	5.0	160	10 Q39425	Q39425 betula verr

93	6	5.0	160	12	Q9YUD4	Q9YUD4 beak and fe	166	6	5.0	232	2	Q9HYC1	Q9HYC1 pseudomonas
94	6	5.0	161	4	Q9HA90	Q9HA90 homo sapien	167	6	5.0	233	4	Q9BYG2	Q9BYG2 homo sapien
95	6	5.0	162	11	Q9CWF7	Q9CWF7 mus musculus	168	6	5.0	234	1	Q9UWR4	Q9UWR4 uncultured
96	6	5.0	163	2	Q99RA6	Q99RA6 staphylococ	169	6	5.0	238	1	Q9Y9V4	Q9Y9V4 aeropyrum p
97	6	5.0	164	3	P78696	P78696 hirsutella	170	6	5.0	239	3	Q9P3C5	Q9P3C5 neopspora
98	6	5.0	168	5	Q9VWMS	Q9VWMS drosophila	171	6	5.0	239	10	O81430	O81430 arabidopsis
99	6	5.0	169	1	Q27584	Q27584 methanobact	172	6	5.0	239	12	Q9QME3	Q9QME3 avian endog
100	6	5.0	173	5	Q93209	Q93209 caenorhabdi	173	6	5.0	240	2	Q9PGT4	Q9PGT4 xylella fas
101	6	5.0	173	5	Q9VXB3	Q9VXB3 drosophila	174	6	5.0	240	5	Q9XUP3	Q9XUP3 caenorhabdi
102	6	5.0	174	10	Q9M3T4	Q9M3T4 betula verr	175	6	5.0	240	13	Q9DEW4	Q9DEW4 raja eglant
103	6	5.0	175	5	Q9G1S5	Q9G1S5 leishmania	176	6	5.0	241	1	Q9HIP9	Q9HIP9 thermoplas
104	6	5.0	177	1	Q29336	Q29336 archaeoglob	177	6	5.0	241	3	Q94436	Q94436 schizosacch
105	6	5.0	179	2	Q44986	Q44986 borrelia af	178	6	5.0	241	12	O11309	O11309 molluscum c
106	6	5.0	179	2	Q44987	Q44987 borrelia af	179	6	5.0	243	10	Q9AX45	Q9AX45 oryza sativ
107	6	5.0	179	2	Q44988	Q44988 borrelia af	180	6	5.0	243	11	Q9CSK3	Q9CSK3 mus musculu
108	6	5.0	179	8	Q9GAG5	Q9GAG5 polyrhachis	181	6	5.0	246	4	O95552	O95552 homo sapien
109	6	5.0	180	2	Q44991	Q44991 borrelia af	182	6	5.0	246	10	O81241	O81241 hellanthus
110	6	5.0	182	2	O84322	O84322 chlamydia t	183	6	5.0	246	10	Q9FS15	Q9FS15 arabidopsis
111	6	5.0	182	2	O84322	O84322 chlamydia t	184	6	5.0	248	2	Q9KED8	Q9KED8 bacillus ha
112	6	5.0	191	1	Q9YFW9	Q9YFW9 aeropyrum p	185	6	5.0	248	11	Q9CWD5	Q9CWD5 mus musculu
113	6	5.0	191	5	Q9N7Z4	Q9N7Z4 leishmania	186	6	5.0	248	13	O12952	O12952 cynops pyrr
114	6	5.0	191	10	O48763	O48763 arabidopsis	187	6	5.0	250	2	Q9KPF0	Q9KPF0 vibrio chol
115	6	5.0	191	10	O82327	O82327 arabidopsis	188	6	5.0	250	4	O9BR29	O9BR29 homo sapien
116	6	5.0	191	10	Q9C5S0	Q9C5S0 arabidopsis	189	6	5.0	251	2	P73200	P73200 synecocyst
117	6	5.0	193	1	Q9HMG4	Q9HMG4 halobacteri	190	6	5.0	251	5	Q22186	Q22186 caenorhabdi
118	6	5.0	193	2	P94226	P94226 borrelia bu	191	6	5.0	253	5	Q9U8V1	Q9U8V1 branchiost
119	6	5.0	193	2	O54433	O54433 l plasmid p	192	6	5.0	258	4	O9H8Q2	O9H8Q2 homo sapien
120	6	5.0	193	2	Q9AC96	Q9AC96 lactococcus	193	6	5.0	258	4	O9BUD2	O9BUD2 homo sapien
121	6	5.0	193	10	O22322	O22322 musa acumin	194	6	5.0	261	2	O9PIF7	O9PIF7 campylobact
122	6	5.0	194	2	Q9S3P4	Q9S3P4 borrelia bu	195	6	5.0	263	2	O9KJ17	O9KJ17 desulfovibr
123	6	5.0	196	10	O48545	O48545 arabidopsis	196	6	5.0	265	2	O9X665	O9X665 staphylococ
124	6	5.0	197	10	O04369	O04369 lotus japon	197	6	5.0	265	8	Q9G925	Q9G925 ochronas
125	6	5.0	197	10	O24142	O24142 nicotiana t	198	6	5.0	266	2	O99Q03	O99Q03 staphylococ
126	6	5.0	197	10	P92978	P92978 arabidopsis	199	6	5.0	267	1	O54654	O54654 halobacteri
127	6	5.0	197	10	Q9SMC3	Q9SMC3 medicago sa	200	6	5.0	267	4	Q9NS99	Q9NS99 homo sapien
128	6	5.0	197	10	O9S820	O9S820 nicotiana t	201	6	5.0	268	10	P81394	P81394 antirrhinum
129	6	5.0	197	10	O65632	O65632 arabidopsis	202	6	5.0	270	2	Q9RP27	Q9RP27 haemophilus
130	6	5.0	198	10	O65062	O65062 picea maria	203	6	5.0	270	2	Q9R2A8	Q9R2A8 mus musculu
131	6	5.0	198	10	Q9ZRD5	Q9ZRD5 arabidopsis	204	6	5.0	271	11	Q9R2A8	Q9R2A8 mus musculu
132	6	5.0	199	2	Q9PEA4	Q9PEA4 xylella fas	205	6	5.0	273	1	O59396	O59396 pyrococcus
133	6	5.0	199	10	O80508	O80508 arabidopsis	206	6	5.0	274	1	O9HIQ7	O9HIQ7 thermoplas
134	6	5.0	202	2	P96506	P96506 borrelia af	207	6	5.0	274	6	Q9GKD9	Q9GKD9 bos taurus
135	6	5.0	203	2	O96623	O96623 borrelia af	208	6	5.0	275	10	Q9S759	Q9S759 kalanchoe f
136	6	5.0	203	2	P96507	P96507 borrelia af	209	6	5.0	276	2	Q9TDM7	Q9TDM7 mesocetoid
137	6	5.0	204	12	Q65843	Q65843 beet wester	210	6	5.0	276	2	P72136	P72136 pseudomonas
138	6	5.0	205	4	Q9WTC7	Q9WTC7 homo sapien	211	6	5.0	278	5	O17254	O17254 caenorhabdi
139	6	5.0	208	10	Q9LQ70	Q9LQ70 arabidopsis	212	6	5.0	279	2	Q9KDB7	Q9KDB7 bacillus ha
140	6	5.0	209	2	O54153	O54153 shigella fl	213	6	5.0	280	2	O99XK1	O99XK1 streptococ
141	6	5.0	209	5	Q9VX73	Q9VX73 drosophila	214	6	5.0	283	1	O28143	O28143 archaeoglob
142	6	5.0	209	10	Q9XGU0	Q9XGU0 arabidopsis	215	6	5.0	283	11	Q9D412	Q9D412 mus musculu
143	6	5.0	211	2	Q49577	Q49577 borrelia af	216	6	5.0	284	10	Q38913	Q38913 arabidopsis
144	6	5.0	212	2	O44669	O44669 borrelia af	217	6	5.0	286	2	Q9PPY5	Q9PPY5 ureaplasma
145	6	5.0	212	2	O9KIM4	O9KIM4 borrelia af	218	6	5.0	289	5	Q21150	Q21150 caenorhabdi
146	6	5.0	212	10	Q9FSN7	Q9FSN7 oryza sativ	219	6	5.0	292	2	O9X2C8	O9X2C8 thermotoga
147	6	5.0	212	11	Q99JH8	Q99JH8 mus musculu	220	6	5.0	292	6	Q9GKE0	Q9GKE0 bos taurus
148	6	5.0	216	8	Q9B8Q1	Q9B8Q1 choloeus d	221	6	5.0	293	2	Q9WY20	Q9WY20 thermotoga
149	6	5.0	219	8	Q9TLT3	Q9TLT3 cyanidium c	222	6	5.0	293	5	Q9XTE9	Q9XTE9 caenorhabdi
150	6	5.0	219	8	Q9B9F8	Q9B9F8 prionodon l	223	6	5.0	294	10	Q39533	Q39533 citrullus l
151	6	5.0	219	10	Q9FXC0	Q9FXC0 arabidopsis	224	6	5.0	294	10	O9LGS3	O9LGS3 oryza sativ
152	6	5.0	220	11	Q9QY18	Q9QY18 mus musculu	225	6	5.0	295	5	O62144	O62144 caenorhabdi
153	6	5.0	221	2	Q91302	Q91302 pseudomonas	226	6	5.0	298	5	O61906	O61906 caenorhabdi
154	6	5.0	223	1	O26710	O26710 methanobact	227	6	5.0	299	11	Q9CW34	Q9CW34 mus musculu
155	6	5.0	223	4	Q9H687	Q9H687 homo sapien	228	6	5.0	300	2	Q9L0L3	Q9L0L3 streptomyce
156	6	5.0	224	3	O01680	O01680 pneumocysti	229	6	5.0	302	2	Q9RZU7	Q9RZU7 deinococcus
157	6	5.0	224	4	O9UJF5	O9UJF5 homo sapien	230	6	5.0	305	2	Q9KWC1	Q9KWC1 agrobacteri
158	6	5.0	225	4	O9BQG9	O9BQG9 homo sapien	231	6	5.0	305	2	O9F0W2	O9F0W2 pseudomonas
159	6	5.0	225	11	Q9DLJ5	Q9DLJ5 mus musculu	232	6	5.0	306	4	O13962	O13962 homo sapien
160	6	5.0	225	11	Q9CUE2	Q9CUE2 mus musculu	233	6	5.0	309	8	O21043	O21043 dictyosteli
161	6	5.0	227	1	Q9HN05	Q9HN05 halobacteri	234	6	5.0	311	2	O34127	O34127 streptococ
162	6	5.0	228	2	Q9L596	Q9L596 heliobacter	235	6	5.0	311	5	Q9V1W8	Q9V1W8 strophophila
163	6	5.0	230	4	O95553	O95553 homo sapien	236	6	5.0	312	4	Q9BUV1	Q9BUV1 homo sapien
164	6	5.0	231	1	P95959	P95959 sulfolobus	237	6	5.0	312	10	Q42538	Q42538 arabidopsis
165	6	5.0	231	8	Q02449	Q02449 chlamydomon	238	6	5.0	312	11	Q9DA41	Q9DA41 mus musculu

239	6	5.0	312	11	Q9CWX7	Q9CWX7 mus musculus	312	10	Q9SAW2	Q9SAW2 arabidopsis
240	6	5.0	314	4	Q9H418	Q9H418 homo sapien	313	2	Q25835	Q25835 helicobacte
241	6	5.0	315	4	Q9P0X8	Q9P0X8 homo sapien	314	2	Q92JY9	Q92JY9 helicobacte
242	6	5.0	316	2	Q9C1M8	Q9C1M8 lactococcus	315	2	Q9RYA6	Q9RYA6 deinococcus
243	6	5.0	317	9	Q38317	Q38317 lactobacilli	316	6	Q9C1Z6	Q9C1Z6 pichia past
244	6	5.0	319	2	Q06448	Q06448 serratia ma	317	6	Q9AZA4	Q9AZA4 lactobacilli
245	6	5.0	319	5	Q9VNJ0	Q9VNJ0 drosophila	318	6	Q14097	Q14097 homo sapien
246	6	5.0	319	10	Q41725	Q41725 zinnia eleg	319	6	Q16951	Q16951 caenorhabdi
247	6	5.0	319	11	Q9QUH4	Q9QUH4 mus musculus	320	6	Q20405	Q20405 felis silve
248	6	5.0	320	2	Q31433	Q31433 bacillus su	321	6	Q20406	Q20406 felis silve
249	6	5.0	320	4	Q9H6U1	Q9H6U1 homo sapien	322	6	Q9NFV3	Q9NFV3 lymnaea sta
250	6	5.0	321	4	Q9H6U1	Q9H6U1 homo sapien	323	6	Q9NFV2	Q9NFV2 lymnaea sta
251	6	5.0	322	4	Q9H6U1	Q9H6U1 homo sapien	324	6	Q9NFV1	Q9NFV1 lymnaea sta
252	6	5.0	325	11	Q61110	Q61110 mus musculus	325	6	Q9NFV0	Q9NFV0 lymnaea sta
253	6	5.0	329	5	Q21738	Q21738 caenorhabdi	326	6	Q9NFV0	Q9NFV0 lymnaea sta
254	6	5.0	329	5	Q9CUE7	Q9CUE7 caenorhabdi	327	6	Q9NFV1	Q9NFV1 lymnaea sta
255	6	5.0	329	10	Q43737	Q43737 arabidopsis	328	6	Q9NFV1	Q9NFV1 lymnaea sta
256	6	5.0	329	10	Q9LSY7	Q9LSY7 arabidopsis	329	6	Q9NFV1	Q9NFV1 lymnaea sta
257	6	5.0	330	2	Q9CM09	Q9CM09 pasteurella	330	6	Q9NFV1	Q9NFV1 lymnaea sta
258	6	5.0	331	4	Q9H6D9	Q9H6D9 homo sapien	331	6	Q9NFV1	Q9NFV1 lymnaea sta
259	6	5.0	331	4	Q9H3H6	Q9H3H6 homo sapien	332	6	Q9NFV1	Q9NFV1 lymnaea sta
260	6	5.0	332	3	Q9P887	Q9P887 candida alb	333	6	Q9NFV1	Q9NFV1 lymnaea sta
261	6	5.0	332	10	Q9SCJ7	Q9SCJ7 arabidopsis	334	6	Q9NFV1	Q9NFV1 lymnaea sta
262	6	5.0	333	2	P74586	P74586 synecocyst	335	6	Q9NFV1	Q9NFV1 lymnaea sta
263	6	5.0	333	6	Q9GM09	Q9GM09 macaca fasc	336	6	Q9NFV1	Q9NFV1 lymnaea sta
264	6	5.0	333	10	Q9CAM7	Q9CAM7 arabidopsis	337	6	Q9NFV1	Q9NFV1 lymnaea sta
265	6	5.0	334	2	Q9CHE1	Q9CHE1 lactococcus	338	6	Q9NFV1	Q9NFV1 lymnaea sta
266	6	5.0	334	2	Q9ABN8	Q9ABN8 caulobacter	339	6	Q9NFV1	Q9NFV1 lymnaea sta
267	6	5.0	336	11	Q9R1S6	Q9R1S6 rattus norv	340	6	Q9NFV1	Q9NFV1 lymnaea sta
268	6	5.0	336	13	Q9DD08	Q9DD08 xenopus lae	341	6	Q9NFV1	Q9NFV1 lymnaea sta
269	6	5.0	337	4	Q9P0X7	Q9P0X7 homo sapien	342	6	Q9NFV1	Q9NFV1 lymnaea sta
270	6	5.0	338	2	Q06452	Q06452 streptococ	343	6	Q9NFV1	Q9NFV1 lymnaea sta
271	6	5.0	338	11	Q88972	Q88972 mus musculus	344	6	Q9NFV1	Q9NFV1 lymnaea sta
272	6	5.0	339	12	Q40645	Q40645 saimirine	345	6	Q9NFV1	Q9NFV1 lymnaea sta
273	6	5.0	340	13	Q9YH20	Q9YH20 gallus gall	346	6	Q9NFV1	Q9NFV1 lymnaea sta
274	6	5.0	341	2	Q9X4N4	Q9X4N4 bacteroides	347	6	Q9NFV1	Q9NFV1 lymnaea sta
275	6	5.0	341	4	Q9P0X6	Q9P0X6 homo sapien	348	6	Q9NFV1	Q9NFV1 lymnaea sta
276	6	5.0	341	6	Q9GMV1	Q9GMV1 canis famil	349	6	Q9NFV1	Q9NFV1 lymnaea sta
277	6	5.0	341	11	Q9QY59	Q9QY59 mus musculus	350	6	Q9NFV1	Q9NFV1 lymnaea sta
278	6	5.0	342	2	Q9A765	Q9A765 caulobacter	351	6	Q9NFV1	Q9NFV1 lymnaea sta
279	6	5.0	342	4	Q9NWK4	Q9NWK4 homo sapien	352	6	Q9NFV1	Q9NFV1 lymnaea sta
280	6	5.0	342	8	Q33761	Q33761 allomyces m	353	6	Q9NFV1	Q9NFV1 lymnaea sta
281	6	5.0	343	2	Q9CHP8	Q9CHP8 lactococcus	354	6	Q9NFV1	Q9NFV1 lymnaea sta
282	6	5.0	344	2	Q9KAP5	Q9KAP5 bacillus ha	355	6	Q9NFV1	Q9NFV1 lymnaea sta
283	6	5.0	344	11	Q9Z246	Q9Z246 mus musculus	356	6	Q9NFV1	Q9NFV1 lymnaea sta
284	6	5.0	345	2	P77585	P77585 escherichia	357	6	Q9NFV1	Q9NFV1 lymnaea sta
285	6	5.0	345	5	Q9W4G3	Q9W4G3 drosophila	358	6	Q9NFV1	Q9NFV1 lymnaea sta
286	6	5.0	345	5	Q9W0R2	Q9W0R2 drosophila	359	6	Q9NFV1	Q9NFV1 lymnaea sta
287	6	5.0	347	2	Q55619	Q55619 synecocyst	360	6	Q9NFV1	Q9NFV1 lymnaea sta
288	6	5.0	347	4	Q9P0Y0	Q9P0Y0 homo sapien	361	6	Q9NFV1	Q9NFV1 lymnaea sta
289	6	5.0	347	10	P93544	P93544 spinacia ol	362	6	Q9NFV1	Q9NFV1 lymnaea sta
290	6	5.0	348	4	Q9BVE3	Q9BVE3 homo sapien	363	6	Q9NFV1	Q9NFV1 lymnaea sta
291	6	5.0	354	5	Q21880	Q21880 caenorhabdi	364	6	Q9NFV1	Q9NFV1 lymnaea sta
292	6	5.0	355	10	Q81242	Q81242 arabidopsis	365	6	Q9NFV1	Q9NFV1 lymnaea sta
293	6	5.0	355	10	Q9SBE7	Q9SBE7 arabidopsis	366	6	Q9NFV1	Q9NFV1 lymnaea sta
294	6	5.0	357	2	Q9P106	Q9P106 campylobact	367	6	Q9NFV1	Q9NFV1 lymnaea sta
295	6	5.0	359	2	Q9H276	Q9H276 pseudomonas	368	6	Q9NFV1	Q9NFV1 lymnaea sta
296	6	5.0	359	10	Q9SPV4	Q9SPV4 clarkia bre	369	6	Q9NFV1	Q9NFV1 lymnaea sta
297	6	5.0	362	11	Q61536	Q61536 mus musculus	370	6	Q9NFV1	Q9NFV1 lymnaea sta
298	6	5.0	363	4	Q9P0X9	Q9P0X9 homo sapien	371	6	Q9NFV1	Q9NFV1 lymnaea sta
299	6	5.0	363	5	Q9VGL8	Q9VGL8 drosophila	372	6	Q9NFV1	Q9NFV1 lymnaea sta
300	6	5.0	364	10	Q23580	Q23580 arabidopsis	373	6	Q9NFV1	Q9NFV1 lymnaea sta
301	6	5.0	365	1	Q9HHX5	Q9HHX5 halobacteri	374	6	Q9NFV1	Q9NFV1 lymnaea sta
302	6	5.0	365	11	Q9D124	Q9D124 mus musculus	375	6	Q9NFV1	Q9NFV1 lymnaea sta
303	6	5.0	366	2	Q45378	Q45378 bordetella	376	6	Q9NFV1	Q9NFV1 lymnaea sta
304	6	5.0	366	2	Q88001	Q88001 bordetella	377	6	Q9NFV1	Q9NFV1 lymnaea sta
305	6	5.0	366	2	Q9L1R0	Q9L1R0 streptomyce	378	6	Q9NFV1	Q9NFV1 lymnaea sta
306	6	5.0	368	10	Q9SXX7	Q9SXX7 nicotiana t	379	6	Q9NFV1	Q9NFV1 lymnaea sta
307	6	5.0	370	2	Q9HHW5	Q9HHW5 pseudomonas	380	6	Q9NFV1	Q9NFV1 lymnaea sta
308	6	5.0	371	11	Q88178	Q88178 rattus norv	381	6	Q9NFV1	Q9NFV1 lymnaea sta
309	6	5.0	372	3	Q06813	Q06813 saccharomyc	382	6	Q9NFV1	Q9NFV1 lymnaea sta
310	6	5.0	372	5	Q9U116	Q9U116 drosophila	383	6	Q9NFV1	Q9NFV1 lymnaea sta
311	6	5.0	372	5	Q9V117	Q9V117 drosophila	384	6	Q9NFV1	Q9NFV1 lymnaea sta

385	6	5.0	439	2	005912	005912 mycobacteri	458	6	5.0	533	2	Q9R2R6	Q9r2r6 ehrlichia e
386	6	5.0	439	5	096569	096569 drosophila	459	6	5.0	535	8	Q9B6E7	Q9b6e7 yarrowia li
387	6	5.0	439	10	Q9FWD4	Q9fwd4 oryza sativ	460	6	5.0	536	13	Q9PW76	Q9pw76 brachydanio
388	6	5.0	440	2	007334	007334 synechococc	461	6	5.0	541	2	008373	008373 ehrlichia s
389	6	5.0	440	5	Q9GN11	Q9gnt1 trypanosoma	462	6	5.0	542	5	Q9W0K7	Q9w0k7 drosophila
390	6	5.0	442	2	Q9X2B5	Q9x2b5 thermotoga	463	6	5.0	543	3	Q9C1C8	Q9c1c8 emericella
391	6	5.0	445	2	Q99Q86	Q99qs6 staphylococ	464	6	5.0	544	4	Q13652	Q13652 homo sapien
392	6	5.0	446	2	Q9PBX6	Q9pbx6 xylella fas	465	6	5.0	546	5	Q9VMT1	Q9vmt1 drosophila
393	6	5.0	446	2	Q99WE4	Q99we4 staphylococ	466	6	5.0	547	2	Q9XAU7	Q9xau7 alteromonas
394	6	5.0	449	12	Q9PZ18	Q9pz18 xestia c-n1	467	6	5.0	549	2	Q9KG93	Q9kg93 bacillus ha
395	6	5.0	453	10	Q9SEW1	Q9sbw1 oryza sativ	468	6	5.0	549	2	Q9AJB5	Q9ajb5 pseudocalter
396	6	5.0	454	4	Q43293	Q43293 homo sapien	469	6	5.0	550	4	Q9HBS2	Q9hbs2 homo sapien
397	6	5.0	454	4	Q9UF99	Q9uf99 homo sapien	470	6	5.0	550	10	Q9LKK0	Q9lkk0 arabidopsis
398	6	5.0	456	5	Q00834	Q00834 toxoplasma	471	6	5.0	551	1	Q9HKN7	Q9hkn7 thermoplasm
399	6	5.0	457	2	Q53488	Q53488 micromonosp	472	6	5.0	555	2	Q9X603	Q9x603 primary end
400	6	5.0	457	10	Q9MAI3	Q9mai3 arabidopsis	473	6	5.0	555	13	Q9W791	Q9w791 xenopus lae
401	6	5.0	459	10	Q9XF48	Q9xf48 arabidopsis	474	6	5.0	556	13	Q9W792	Q9w792 brachydanio
402	6	5.0	459	11	Q9JJA1	Q9jja1 mus musculu	475	6	5.0	557	10	Q9SF16	Q9sf16 arabidopsis
403	6	5.0	459	11	Q9CYQ0	Q9cyq0 mus musculu	476	6	5.0	557	12	Q9WR11	Q9wrt1 macaca mula
404	6	5.0	461	2	Q9K498	Q9k498 streptomyce	477	6	5.0	557	12	Q9J2L5	Q9j2l5 macaca mula
405	6	5.0	462	8	Q9BAD4	Q9bad4 brassica na	478	6	5.0	558	5	Q9VJX7	Q9vjx7 drosophila
406	6	5.0	463	13	Q9PW75	Q9pw75 brachydanio	479	6	5.0	560	11	Q9EP84	Q9ep84 mus musculu
407	6	5.0	463	13	Q9PW74	Q9pw74 brachydanio	480	6	5.0	561	12	Q9DK05	Q9dk05 allpahuayo
408	6	5.0	468	2	Q9LAI1	Q9lai1 salmonella	481	6	5.0	561	12	Q9DK04	Q9dk04 allpahuayo
409	6	5.0	469	4	Q14573	Q14573 homo sapien	482	6	5.0	563	5	Q24326	Q24326 drosophila
410	6	5.0	470	2	Q9KAH9	Q9kah9 bacillus ha	483	6	5.0	563	5	Q27933	Q27933 drosophila
411	6	5.0	470	5	Q9VIQ2	Q9viq2 drosophila	484	6	5.0	564	4	Q9BKN4	Q9bkn4 homo sapien
412	6	5.0	472	5	Q20406	Q20406 caenorhabdi	485	6	5.0	565	4	Q9UBW5	Q9ubw5 homo sapien
413	6	5.0	474	5	Q9VQ69	Q9vq69 drosophila	486	6	5.0	565	5	Q21615	Q21615 caenorhabdi
414	6	5.0	475	2	Q9A592	Q9a592 caulobacter	487	6	5.0	568	10	Q9SXD0	Q9sxd0 arabidopsis
415	6	5.0	476	10	P93023	P93023 arabidopsis	488	6	5.0	569	4	Q9BW49	Q9bw49 homo sapien
416	6	5.0	477	10	Q9XID1	Q9xid1 arabidopsis	489	6	5.0	569	11	Q9D0R1	Q9d0r1 mus musculu
417	6	5.0	477	10	Q9FVH4	Q9fvh4 arabidopsis	490	6	5.0	570	4	Q9H6M6	Q9hm66 homo sapien
418	6	5.0	481	3	Q94615	Q94615 schizosacch	491	6	5.0	573	5	Q9GQ09	Q9gqu9 caenorhabdi
419	6	5.0	482	9	Q36165	Q36165 bacterioph	492	6	5.0	576	11	Q70295	Q70295 mus musculu
420	6	5.0	483	10	Q9FL69	Q9fl69 arabidopsis	493	6	5.0	576	11	P97548	P97548 rattus norv
421	6	5.0	484	2	Q56770	Q56770 xanthomonas	494	6	5.0	584	10	Q9SPU1	Q9spu1 oryza sativ
422	6	5.0	485	10	Q65475	Q65475 arabidopsis	495	6	5.0	589	4	Q60541	Q60541 homo sapien
423	6	5.0	487	2	Q9KJX4	Q9kjsx4 myxococcus	496	6	5.0	589	11	Q70296	Q70296 mus musculu
424	6	5.0	491	4	Q9UK46	Q9uk46 homo sapien	497	6	5.0	589	11	P97549	P97549 rattus norv
425	6	5.0	491	6	Q29516	Q29516 cryctolagus	498	6	5.0	590	3	Q42631	Q42631 emericella
426	6	5.0	491	6	Q29532	Q29532 cryctolagus	499	6	5.0	590	3	P93022	P93022 arabidopsis
427	6	5.0	491	11	Q9WUD0	Q9wud0 mus musculu	500	6	5.0	591	10	Q9SG12	Q9sg12 arabidopsis
428	6	5.0	491	11	Q64463	Q64463 mus musculu	501	6	5.0	594	10	Q9FTM9	Q9ftm9 arabidopsis
429	6	5.0	491	11	Q64460	Q64460 mus musculu	502	6	5.0	594	10	Q9FV63	Q9fcv3 mus musculu
430	6	5.0	491	11	Q64584	Q64584 rattus norv	503	6	5.0	596	11	Q9VTL3	Q9vtl3 drosophila
431	6	5.0	494	11	Q9JJC0	Q9jjc0 rattus norv	504	6	5.0	598	2	Q83032	Q83032 streptomyce
432	6	5.0	496	9	Q9TIC0	Q9tic0 bacterioph	505	6	5.0	599	2	Q9L0I0	Q9l0i0 streptomyce
433	6	5.0	497	5	Q44704	Q44704 caenorhabdi	506	6	5.0	602	2	Q84593	Q84593 chlamydia t
434	6	5.0	499	2	Q9JVT1	Q9jvt1 neisseria m	507	6	5.0	602	2	Q9PJT1	Q9pjf1 chlamydia m
435	6	5.0	502	2	Q9KSU5	Q9ksu5 vibrio chol	508	6	5.0	602	4	Q9H5H5	Q9h5h5 homo sapien
436	6	5.0	502	11	Q9DBF3	Q9dbf3 mus musculu	509	6	5.0	604	13	Q42472	Q42472 xenopus lae
437	6	5.0	503	12	Q39779	Q39779 equine herp	510	6	5.0	605	5	Q45302	Q45302 caenorhabdi
438	6	5.0	504	8	Q9MCX9	Q9mcx9 picumnus au	511	6	5.0	605	11	Q62224	Q62224 mus musculu
439	6	5.0	507	2	Q48707	Q48707 lactobacill	512	6	5.0	608	8	Q9B6E6	Q9b6e6 yarrowia li
440	6	5.0	507	5	Q45291	Q45291 caenorhabdi	513	6	5.0	611	2	Q9KLZ8	Q9klz8 vibrio chol
441	6	5.0	507	12	Q9J8C8	Q9j8c8 spodoptera	514	6	5.0	611	5	Q9VY64	Q9vy64 drosophila
442	6	5.0	508	4	Q9BS53	Q9bs53 homo sapien	515	6	5.0	620	5	Q9VTH3	Q9vth3 drosophila
443	6	5.0	509	2	Q9PC94	Q9pc94 xylella fas	516	6	5.0	621	2	Q9I2T8	Q9i2t8 pseudomonas
444	6	5.0	510	5	Q9VIZ8	Q9viz8 drosophila	517	6	5.0	621	4	Q9BTR2	Q9btr2 homo sapien
445	6	5.0	511	2	Q9RY57	Q9ry57 deinococcus	518	6	5.0	622	4	Q14859	Q14859 homo sapien
446	6	5.0	513	2	Q9KVQ7	Q9kvq7 vibrio chol	519	6	5.0	623	5	Q9VNO6	Q9vng6 drosophila
447	6	5.0	513	3	Q9P6A1	Q9p6a1 neurospora	520	6	5.0	624	11	Q9D2G7	Q9d2g7 mus musculu
448	6	5.0	515	2	Q9XD06	Q9xd06 desulfitoba	521	6	5.0	625	4	Q14677	Q14677 homo sapien
449	6	5.0	516	12	Q56283	Q56283 human herpe	522	6	5.0	628	10	Q9SF51	Q9sf51 arabidopsis
450	6	5.0	519	2	Q9PCG3	Q9pcg3 xylella fas	523	6	5.0	630	4	Q9BR17	Q9br17 homo sapien
451	6	5.0	527	10	Q9LET6	Q9let6 arabidopsis	524	6	5.0	630	10	Q9LZU6	Q9lzu6 arabidopsis
452	6	5.0	527	12	Q9YTP5	Q9ytp5 ateline her	525	6	5.0	635	2	Q9JTR6	Q9jtr6 neisseria m
453	6	5.0	530	2	Q9PNC0	Q9pnc0 campylobact	526	6	5.0	640	5	Q9Y3W8	Q9y3w8 homo sapien
454	6	5.0	530	2	Q9AA00	Q9aa00 caulobacter	527	6	5.0	647	5	Q9V9T1	Q9v9t1 drosophila
455	6	5.0	531	11	Q99KN9	Q99kn9 mus musculu	528	6	5.0	651	2	Q9RD10	Q9rd10 streptomyce
456	6	5.0	533	2	Q9S3V5	Q9s3v5 ehrlichia e	529	6	5.0	654	10	Q9ZV25	Q9zv25 arabidopsis
457	6	5.0	533	2	Q9R2R7	Q9r2r7 ehrlichia s	530	6	5.0	656	4	Q9P0U4	Q9p0u4 homo sapien

531	6	5.0	656	4	Q9P2V7	Q9p2v7 homo sapien	604	890	10	Q9LJS0	Q9ljs0 arabidopsis
532	6	5.0	660	11	Q9CWM7	Q9cwm7 mus musculus	605	896	2	Q52618	Q52618 pseudomonas
533	6	5.0	663	8	Q9B6E5	Q9b6e5 yarrowia li	606	896	2	Q52618	Q52618 pseudomonas
534	6	5.0	663	12	Q9B188	Q9b188 molluscum c	607	901	12	P72250	P72250 rhodospirillum rubrum
535	6	5.0	670	2	Q32212	Q32212 bacillus su	608	901	12	Q908K1	Q908k1 myxoma viru
536	6	5.0	670	4	Q9P1S9	Q9p1s9 homo sapien	609	902	12	Q908X9	Q908x9 shope fibro
537	6	5.0	670	5	Q77423	Q77423 bacterocera	610	905	10	Q9WIT8	Q9wit8 drosophila
538	6	5.0	671	2	Q9HT84	Q9ht84 pseudomonas	611	907	10	Q9C946	Q9c946 arabidopsis
539	6	5.0	671	10	Q9SKK5	Q9skk5 arabidopsis	612	922	5	Q46354	Q46354 caenorhabdi
540	6	5.0	672	4	Q9NV14	Q9nv14 homo sapien	613	927	3	Q9C946	Q9c946 arabidopsis
541	6	5.0	684	4	Q9UF31	Q9uf31 homo sapien	614	927	3	Q9C946	Q9c946 arabidopsis
542	6	5.0	686	10	Q9STM2	Q9stm2 arabidopsis	615	927	3	Q9C946	Q9c946 arabidopsis
543	6	5.0	689	5	Q97020	Q97020 octopus dof	616	927	3	Q9C946	Q9c946 arabidopsis
544	6	5.0	689	5	Q9N2R0	Q9n2r0 loligo peal	617	927	3	Q9C946	Q9c946 arabidopsis
545	6	5.0	690	10	Q9SKC6	Q9skc6 arabidopsis	618	927	3	Q9C946	Q9c946 arabidopsis
546	6	5.0	692	2	Q30565	Q30565 bacillus br	619	927	3	Q9C946	Q9c946 arabidopsis
547	6	5.0	695	8	Q20159	Q20159 chlorella v	620	927	3	Q9C946	Q9c946 arabidopsis
548	6	5.0	698	10	Q9SDA9	Q9sda9 arabidopsis	621	927	3	Q9C946	Q9c946 arabidopsis
549	6	5.0	701	2	Q9KG92	Q9kg92 bacillus ha	622	927	3	Q9C946	Q9c946 arabidopsis
550	6	5.0	702	5	Q9VFE8	Q9vfe8 drosophila	623	927	3	Q9C946	Q9c946 arabidopsis
551	6	5.0	706	5	Q9VYR5	Q9vyr5 drosophila	624	927	3	Q9C946	Q9c946 arabidopsis
552	6	5.0	711	4	Q15462	Q15462 homo sapien	625	927	3	Q9C946	Q9c946 arabidopsis
553	6	5.0	714	4	Q9HBF9	Q9hbf9 homo sapien	626	927	3	Q9C946	Q9c946 arabidopsis
554	6	5.0	720	10	Q9LDM9	Q9ldm9 nicotiana t	627	927	3	Q9C946	Q9c946 arabidopsis
555	6	5.0	723	5	Q9V9P5	Q9v9p5 drosophila	628	927	3	Q9C946	Q9c946 arabidopsis
556	6	5.0	727	10	Q9SCF0	Q9scf0 datura stra	629	927	3	Q9C946	Q9c946 arabidopsis
557	6	5.0	737	5	Q23985	Q23985 drosophila	630	927	3	Q9C946	Q9c946 arabidopsis
558	6	5.0	738	5	Q9A3Z1	Q9a3z1 drosophila	631	927	3	Q9C946	Q9c946 arabidopsis
559	6	5.0	746	6	Q9RTU3	Q9rtu3 caenorhabdi	632	927	3	Q9C946	Q9c946 arabidopsis
560	6	5.0	746	6	Q9GKE7	Q9gke7 sus scrofa	633	927	3	Q9C946	Q9c946 arabidopsis
561	6	5.0	746	6	Q9GKE7	Q9gke7 sus scrofa	634	927	3	Q9C946	Q9c946 arabidopsis
562	6	5.0	746	6	Q9GKE7	Q9gke7 sus scrofa	635	927	3	Q9C946	Q9c946 arabidopsis
563	6	5.0	746	6	Q9GKE7	Q9gke7 sus scrofa	636	927	3	Q9C946	Q9c946 arabidopsis
564	6	5.0	751	2	Q9HV01	Q9hv01 ranid herpe	637	927	3	Q9C946	Q9c946 arabidopsis
565	6	5.0	752	2	Q9PEZ5	Q9pez5 xylella fas	638	927	3	Q9C946	Q9c946 arabidopsis
566	6	5.0	760	10	Q9ZU97	Q9zu97 arabidopsis	639	927	3	Q9C946	Q9c946 arabidopsis
567	6	5.0	761	10	Q9SUH4	Q9suh4 arabidopsis	640	927	3	Q9C946	Q9c946 arabidopsis
568	6	5.0	761	10	Q9SUH4	Q9suh4 arabidopsis	641	927	3	Q9C946	Q9c946 arabidopsis
569	6	5.0	770	12	Q98XW9	Q98xw9 emeria bru	642	927	3	Q9C946	Q9c946 arabidopsis
570	6	5.0	772	10	Q9LSB4	Q9lsb4 arabidopsis	643	927	3	Q9C946	Q9c946 arabidopsis
571	6	5.0	780	3	Q9UVF2	Q9uvf2 yarrowia li	644	927	3	Q9C946	Q9c946 arabidopsis
572	6	5.0	782	4	Q9BZ14	Q9bz14 homo sapien	645	927	3	Q9C946	Q9c946 arabidopsis
573	6	5.0	784	5	Q9GFW0	Q9gfw0 caenorhabdi	646	927	3	Q9C946	Q9c946 arabidopsis
574	6	5.0	793	5	Q9UGB7	Q9ugb7 caenorhabdi	647	927	3	Q9C946	Q9c946 arabidopsis
575	6	5.0	797	4	Q9UQM5	Q9uqm5 homo sapien	648	927	3	Q9C946	Q9c946 arabidopsis
576	6	5.0	800	10	Q49327	Q49327 arabidopsis	649	927	3	Q9C946	Q9c946 arabidopsis
577	6	5.0	800	11	Q62037	Q62037 mus musculus	650	927	3	Q9C946	Q9c946 arabidopsis
578	6	5.0	801	2	Q9EUI6	Q9eui6 salmonella	651	927	3	Q9C946	Q9c946 arabidopsis
579	6	5.0	802	2	Q9EUK1	Q9euk1 salmonella	652	927	3	Q9C946	Q9c946 arabidopsis
580	6	5.0	803	2	Q9CIW5	Q9ciw5 lactococcus	653	927	3	Q9C946	Q9c946 arabidopsis
581	6	5.0	808	13	Q13080	Q13080 xenopus lae	654	927	3	Q9C946	Q9c946 arabidopsis
582	6	5.0	808	13	Q9PWK7	Q9pwk7 xenopus lae	655	927	3	Q9C946	Q9c946 arabidopsis
583	6	5.0	809	2	Q9R245	Q9rz45 deinococcus	656	927	3	Q9C946	Q9c946 arabidopsis
584	6	5.0	810	2	Q9CFD3	Q9cf3 lactococcus	657	927	3	Q9C946	Q9c946 arabidopsis
585	6	5.0	820	2	Q9KUC1	Q9kuc1 vibrio chol	658	927	3	Q9C946	Q9c946 arabidopsis
586	6	5.0	823	2	Q24895	Q24895 helicobacte	659	927	3	Q9C946	Q9c946 arabidopsis
587	6	5.0	824	2	Q9AAE5	Q9aae5 caulobacter	660	927	3	Q9C946	Q9c946 arabidopsis
588	6	5.0	831	10	Q64781	Q64781 arabidopsis	661	927	3	Q9C946	Q9c946 arabidopsis
589	6	5.0	835	5	Q23122	Q23122 caenorhabdi	662	927	3	Q9C946	Q9c946 arabidopsis
590	6	5.0	837	3	Q9HFV8	Q9hfv8 colletotric	663	927	3	Q9C946	Q9c946 arabidopsis
591	6	5.0	839	5	Q9BHC2	Q9bhq2 leishmania	664	927	3	Q9C946	Q9c946 arabidopsis
592	6	5.0	840	5	Q9N305	Q9n305 caenorhabdi	665	927	3	Q9C946	Q9c946 arabidopsis
593	6	5.0	848	5	Q9V889	Q9v889 drosophila	666	927	3	Q9C946	Q9c946 arabidopsis
594	6	5.0	849	10	Q9SDB0	Q9sdb0 arabidopsis	667	927	3	Q9C946	Q9c946 arabidopsis
595	6	5.0	853	4	Q9BWH5	Q9bwh5 homo sapien	668	927	3	Q9C946	Q9c946 arabidopsis
596	6	5.0	856	12	Q41539	Q41539 human immun	669	927	3	Q9C946	Q9c946 arabidopsis
597	6	5.0	857	2	Q9KXZ5	Q9kxz5 streptomyce	670	927	3	Q9C946	Q9c946 arabidopsis
598	6	5.0	864	10	Q49329	Q49329 arabidopsis	671	927	3	Q9C946	Q9c946 arabidopsis
599	6	5.0	881	10	Q9LJS2	Q9ljs2 arabidopsis	672	927	3	Q9C946	Q9c946 arabidopsis
600	6	5.0	881	12	Q84735	Q84735 phocine her	673	927	3	Q9C946	Q9c946 arabidopsis
601	6	5.0	883	10	Q9LRW9	Q9lrw9 arabidopsis	674	927	3	Q9C946	Q9c946 arabidopsis
602	6	5.0	889	4	Q14917	Q14917 homo sapien	675	927	3	Q9C946	Q9c946 arabidopsis
603	6	5.0	890	10	Q48849	Q48849 arabidopsis	676	927	3	Q9C946	Q9c946 arabidopsis

677	6	5.0	1255	4	Q9BQG0	Q9bqg0 homo sapien	750	6	5.0	3534	12	Q39266	Q39266 equine herp
678	6	5.0	1266	10	Q9LSH3	Q9lsh3 arabidopsis	751	6	5.0	3734	5	Q9BI48	Q9bi48 caenorhabdi
679	6	5.0	1268	10	Q9LUG0	Q9lugo arabidopsis	752	6	5.0	3908	5	Q9BK91	Q9bk91 strongyloce
680	6	5.0	1272	11	Q9TK64	Q9tk64 rattus norv	753	6	5.0	4146	13	Q9BE11	Q9be11 xenopus lae
681	6	5.0	1286	5	P90936	P90936 caenorhabdi	754	6	5.0	7257	2	Q9LC87	Q9lc87 polyanglum
682	6	5.0	1295	3	O13348	O13348 magnaporthe	755	6	5.0	7257	2	Q9KI27	Q9ki27 pseudomonas
683	6	5.0	1304	5	Q96959	Q96959 drosophila	756	6	5.0	9376	2	O85168	O85168 pseudomonas
684	6	5.0	1307	5	Q22670	Q22670 caenorhabdi	757	6	5.0	9507	2	Q9EWA1	Q9ewa1 streptomyce
685	6	5.0	1327	4	Q94897	Q94897 homo sapien	758	5	4.1	16	4	Q9UC55	Q9uc55 homo sapien
686	6	5.0	1336	5	Q9VH43	Q9vhw43 drosophila	759	5	4.1	18	2	Q9F581	Q9f581 escherichia
687	6	5.0	1367	5	Q9VY47	Q9vy47 drosophila	760	5	4.1	20	2	Q46499	Q46499 desulfovibr
688	6	5.0	1371	12	Q9YTP1	Q9ytp1 ateline her	761	5	4.1	21	11	Q9QUX3	Q9qux3 rattus sp.
689	6	5.0	1377	4	Q9P2A8	Q9p2a8 homo sapien	762	5	4.1	21	12	Q84198	Q84198 paramyxovir
690	6	5.0	1397	10	Q9LFP0	Q9lpf0 arabidopsis	763	5	4.1	24	7	Q77868	Q77868 oreochromis
691	6	5.0	1405	10	Q9LHK8	Q9lhk8 arabidopsis	764	5	4.1	24	7	O77869	O77869 oreochromis
692	6	5.0	1413	10	Q9ZUT8	Q9zut8 arabidopsis	765	5	4.1	24	7	O77870	O77870 oreochromis
693	6	5.0	1421	10	O80907	O80907 arabidopsis	766	5	4.1	27	5	Q9BM73	Q9bm73 drosophila
694	6	5.0	1445	10	Q9LRY4	Q9lry4 arabidopsis	767	5	4.1	27	12	O56511	O56511 hepatitis c
695	6	5.0	1446	11	Q9QXC1	Q9qxc1 arabidopsis	768	5	4.1	27	12	O56530	O56530 hepatitis c
696	6	5.0	1450	12	O65974	O65974 mus musculu	769	5	4.1	28	12	Q9QC46	Q9qc46 hepatitis c
697	6	5.0	1450	10	Q9LPH0	Q9lph0 arabidopsis	770	5	4.1	28	12	Q9QC35	Q9qc35 hepatitis c
698	6	5.0	1456	12	Q9IMP2	Q9imp2 potato viru	771	5	4.1	29	8	Q9G636	Q9g636 calotes lio
699	6	5.0	1504	4	Q9UES6	Q9ues6 homo sapien	772	5	4.1	29	8	Q9G633	Q9g633 calotes nig
700	6	5.0	1510	5	O61802	O61802 caenorhabdi	773	5	4.1	29	8	Q9G600	Q9g600 acanthosaur
701	6	5.0	1519	2	O48237	O48237 helicobacte	774	5	4.1	30	4	O14579	O14579 homo sapien
702	6	5.0	1528	4	Q9Y211	Q9y211 homo sapien	775	5	4.1	30	4	Q9UC99	Q9uc99 homo sapien
703	6	5.0	1533	4	O60328	O60328 homo sapien	776	5	4.1	30	5	Q9BM72	Q9bm72 drosophila
704	6	5.0	1547	5	O01940	O01940 drosophila	777	5	4.1	31	10	Q9SMK4	Q9smk4 cicier ariet
705	6	5.0	1547	5	Q9VVF7	Q9vvf7 drosophila	778	5	4.1	33	8	O46929	O46929 joinvillea
706	6	5.0	1569	5	O00820	O00820 acanthamoeb	779	5	4.1	34	8	Q9MFM3	Q9mfm3 leopardus p
707	6	5.0	1604	13	Q90662	Q90662 gallus gall	780	5	4.1	35	8	Q9RPM1	Q9rpm1 puma concol
708	6	5.0	1622	11	Q9Z330	Q9z330 rattus ratt	781	5	4.1	35	8	Q9RPM0	Q9rpm0 bacillus me
709	6	5.0	1685	4	Q9UEM8	Q9uem8 homo sapien	782	5	4.1	35	8	Q33825	Q33825 anas platyr
710	6	5.0	1703	13	Q980F7	Q98uf7 fuqu rubrip	783	5	4.1	38	11	Q99N61	Q99n61 rattus norv
711	6	5.0	1711	5	O45409	O45409 caenorhabdi	784	5	4.1	40	10	Q9S927	Q9s927 carpinus be
712	6	5.0	1713	5	Q9V3Q9	Q9v3q9 drosophila	785	5	4.1	41	8	Q9BAl1	Q9bali hordeum vul
713	6	5.0	1713	5	O96960	O96960 drosophila	786	5	4.1	42	2	O50353	O50353 mycoplasma
714	6	5.0	1724	5	O96960	O96960 drosophila	787	5	4.1	42	2	Q9R898	Q9r898 chlamydia t
715	6	5.0	1738	12	Q39735	Q39735 friend muri	788	5	4.1	42	11	Q9CU49	Q9cu49 mus musculu
716	6	5.0	1752	5	Q9UAK9	Q9uak9 drosophila	789	5	4.1	43	5	O18612	O18612 anemonia su
717	6	5.0	1768	5	Q24153	Q24153 drosophila	790	5	4.1	43	12	Q9Q9X1	Q9q9x1 rift valley
718	6	5.0	1784	10	Q9C6R1	Q9c6r1 arabidopsis	791	5	4.1	43	12	Q9Q9X0	Q9q9x0 rift valley
719	6	5.0	1807	4	Q9ULH6	Q9ulh6 homo sapien	792	5	4.1	43	12	Q9Q9W9	Q9q9w9 rift valley
720	6	5.0	1810	5	Q9V483	Q9v483 drosophila	793	5	4.1	43	12	Q9Q9W8	Q9q9w8 rift valley
721	6	5.0	1814	5	Q9BLM9	Q9blm9 toxocara ca	794	5	4.1	43	12	Q9Q9W7	Q9q9w7 rift valley
722	6	5.0	1872	5	O17083	O17083 athalia ros	795	5	4.1	43	12	Q9Q9W6	Q9q9w6 rift valley
723	6	5.0	1963	5	O02244	O02244 caenorhabdi	796	5	4.1	43	12	Q9Q9W5	Q9q9w5 rift valley
724	6	5.0	1967	5	Q9VPM1	Q9vpm1 drosophila	797	5	4.1	43	12	Q9Q9W4	Q9q9w4 rift valley
725	6	5.0	2126	11	Q9UIH7	Q9jih7 rattus norv	798	5	4.1	43	12	Q9Q9W3	Q9q9w3 rift valley
726	6	5.0	2127	12	O57294	O57294 rabies viru	799	5	4.1	43	12	Q9Q9W2	Q9q9w2 rift valley
727	6	5.0	2127	12	Q9JH63	Q9jh63 rabies viru	800	5	4.1	43	12	Q9Q9W1	Q9q9w1 rift valley
728	6	5.0	2127	12	Q9TPJ5	Q9tpj5 rabies viru	801	5	4.1	43	12	Q9Q9W0	Q9q9w0 rift valley
729	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	802	5	4.1	43	12	Q9Q9V9	Q9q9v9 rift valley
730	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	803	5	4.1	43	12	Q9Q9V8	Q9q9v8 rift valley
731	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	804	5	4.1	43	12	Q9Q9V7	Q9q9v7 rift valley
732	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	805	5	4.1	43	12	Q9Q9V6	Q9q9v6 rift valley
733	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	806	5	4.1	43	12	Q9Q9V5	Q9q9v5 rift valley
734	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	807	5	4.1	43	12	Q9Q9V4	Q9q9v4 rift valley
735	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	808	5	4.1	43	12	Q9Q9V3	Q9q9v3 rift valley
736	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	809	5	4.1	43	12	Q9Q9V2	Q9q9v2 rift valley
737	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	810	5	4.1	43	12	Q9Q9V1	Q9q9v1 rift valley
738	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	811	5	4.1	43	12	Q9Q9V0	Q9q9v0 rift valley
739	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	812	5	4.1	43	12	Q9Q9V9	Q9q9v9 rift valley
740	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	813	5	4.1	43	12	Q9Q9V8	Q9q9v8 rift valley
741	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	814	5	4.1	43	12	Q9Q9V7	Q9q9v7 rift valley
742	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	815	5	4.1	43	12	Q9Q9V6	Q9q9v6 rift valley
743	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	816	5	4.1	43	12	Q9Q9V5	Q9q9v5 rift valley
744	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	817	5	4.1	43	12	Q9Q9V4	Q9q9v4 rift valley
745	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	818	5	4.1	43	12	Q9Q9V3	Q9q9v3 rift valley
746	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	819	5	4.1	43	12	Q9Q9V2	Q9q9v2 rift valley
747	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	820	5	4.1	43	12	Q9Q9V1	Q9q9v1 rift valley
748	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	821	5	4.1	43	12	Q9Q9V0	Q9q9v0 rift valley
749	6	5.0	2131	10	Q9M3I2	Q9m3i2 spinacia ol	822	5	4.1	43	12	Q9Q9V9	Q9q9v9 rift valley

823	5	4.1	51	1	Q9HH93	Q9hh93 sulfobus	896	5	4.1	76	2	Q49255	mycoplasma
824	5	4.1	51	2	Q9KIH8	Q9kih8 rhizobium h	897	5	4.1	76	4	Q9UEF4	Q9uef4 homo sapien
825	5	4.1	51	8	Q9MTI3	Q9mti3 oenothera m	898	5	4.1	76	4	Q9H375	Q9h375 homo sapien
826	5	4.1	51	11	Q63905	Q63905 rattus norv	899	5	4.1	76	10	Q9M689	Q9m689 gossypium h
827	5	4.1	52	2	Q9P0F0	Q9pd0f xylella fas	900	5	4.1	76	10	Q9M686	Q9m686 gossypium h
828	5	4.1	52	12	Q92316	Q92316 human respi	901	5	4.1	76	13	Q9IB49	Q9ib49 pagrus majo
829	5	4.1	52	12	Q92320	Q92320 human respi	902	5	4.1	77	2	Q9H664	Q9h664 streptomyc
830	5	4.1	53	2	Q9P8X9	Q9pbx9 xylella fas	903	5	4.1	77	2	Q9SA43	Q9sa43 escherichia
831	5	4.1	53	5	Q9N706	Q9n706 leishmania	904	5	4.1	77	10	Q64565	Q64565 arabidopsis
832	5	4.1	53	14	Q99IS7	Q99is7 unclutered	905	5	4.1	77	10	Q64565	Q64565 arabidopsis
833	5	4.1	54	2	Q9JVE1	Q9jve1 neisseria m	906	5	4.1	78	1	Q64912	Q64912 lycopersico
834	5	4.1	54	2	Q9JVE1	Q9jve1 neisseria m	906	5	4.1	78	1	Q64912	Q64912 lycopersico
835	5	4.1	54	2	Q9JVE1	Q9jve1 neisseria m	906	5	4.1	78	1	Q64912	Q64912 lycopersico
836	5	4.1	55	4	Q9UGF2	Q9ugf2 homo sapien	907	5	4.1	78	1	Q9V2Y7	Q9v2y7 methanobact
837	5	4.1	55	8	Q9UGF2	Q9ugf2 homo sapien	908	5	4.1	78	2	P73144	synecocyst
838	5	4.1	55	11	Q63761	Q63761 rattus norv	909	5	4.1	78	2	Q9KC16	synecocyst
839	5	4.1	56	11	Q9CTK9	Q9ctk9 mus musculu	910	5	4.1	78	3	Q9HGF5	Q9hgf5 bacillus ha
840	5	4.1	56	13	Q9PSR7	Q9psr7 mus musculu	911	5	4.1	78	11	Q63082	Q63082 rattus norv
841	5	4.1	57	2	Q9K1F2	Q9ksr7 gallus gall	912	5	4.1	78	11	Q63082	Q63082 rattus norv
842	5	4.1	57	2	Q9K1F2	Q9ksr7 gallus gall	912	5	4.1	78	11	Q63082	Q63082 rattus norv
843	5	4.1	57	10	Q9M3J3	Q9m3j3 spinacia ol	913	5	4.1	79	2	Q9JLI5	Q9jli5 rattus norv
844	5	4.1	57	12	Q69114	Q69114 human herpe	914	5	4.1	79	2	Q9ZL89	Q9zlj5 rattus norv
845	5	4.1	57	12	Q69122	Q69122 human herpe	915	5	4.1	79	2	Q9X3N6	Q9x3n6 helicobacte
846	5	4.1	58	6	Q9GLG5	Q9qlc5 ovis aries	916	5	4.1	79	2	Q9WT7F	Q9wt7f escherichia
847	5	4.1	58	10	Q41336	Q41336 lycopersico	917	5	4.1	79	2	Q9JMR3	Q9jmr3 escherichia
848	5	4.1	59	2	Q31552	Q31552 bacillus su	918	5	4.1	79	2	Q9A6Y2	Q9a6y2 caulobacter
849	5	4.1	60	8	Q35497	Q35497 paracentrot	919	5	4.1	79	11	Q9A188	Q9a188 streptococc
850	5	4.1	61	2	P73064	P73064 synecocyst	920	5	4.1	79	11	Q922U6	Q922u6 mus musculu
851	5	4.1	61	2	Q9K9L2	Q9k9l2 bacillus ha	921	5	4.1	80	4	Q9BWR8	Q9bwr8 homo sapien
852	5	4.1	61	11	Q9WVQ2	Q9wvq2 rattus norv	922	5	4.1	80	9	Q9G013	Q9g013 bacterioph
853	5	4.1	62	4	Q15952	Q15952 homo sapien	923	5	4.1	80	10	Q9S963	Q9s963 carpinus be
854	5	4.1	62	4	Q9NR14	Q9nr14 homo sapien	924	5	4.1	80	10	Q9S962	Q9s962 carpinus be
855	5	4.1	62	5	Q9T2S8	Q9t2s8 plasmodium	925	5	4.1	80	12	Q84629	Q84629 paramecium
856	5	4.1	62	5	Q9T2S8	Q9t2s8 plasmodium	926	5	4.1	80	12	Q9YVZ7	Q9yvz7 melanoplus
857	5	4.1	62	5	Q9T2S8	Q9t2s8 plasmodium	927	5	4.1	81	2	Q9Z4Y2	Q9z4y2 streptomyc
858	5	4.1	63	12	Q72145	Q72145 hantavirus	928	5	4.1	81	2	Q9K929	Q9k929 bacillus ha
859	5	4.1	63	12	Q72147	Q72147 hantavirus	929	5	4.1	81	2	Q9K929	Q9k929 bacillus ha
860	5	4.1	64	2	Q9PEP6	Q9pep6 xylella fas	930	5	4.1	81	2	Q9ARW8	Q9arw8 shigella fl
861	5	4.1	64	11	Q9Z2S4	Q9z2s4 rattus norv	931	5	4.1	82	1	Q27686	Q27686 methanobact
862	5	4.1	64	12	Q90775	Q90775 human herpe	932	5	4.1	82	1	Q9HPU0	Q9hpu0 halobacteri
863	5	4.1	65	2	Q9RDI8	Q9rdi8 streptomyc	933	5	4.1	82	2	Q9X3N4	Q9x3n4 bruceella ab
864	5	4.1	65	10	Q43851	Q43851 triticum ae	934	5	4.1	82	5	Q17981	Q17981 caenorhabdi
865	5	4.1	65	10	Q9C6P0	Q9cep0 arabidopsis	935	5	4.1	82	7	Q31433	Q31433 melanochrom
866	5	4.1	65	11	Q61157	Q61157 mus musculu	936	5	4.1	82	7	Q31440	Q31440 melanochrom
867	5	4.1	66	2	P71462	P71462 lactobacilli	937	5	4.1	82	7	Q31450	Q31450 melanochrom
868	5	4.1	66	6	Q9BEF0	Q9bef0 erinaceus e	938	5	4.1	82	7	Q31450	Q31450 melanochrom
869	5	4.1	67	1	P94120	P94120 acidianus a	939	5	4.1	82	7	Q31455	Q31455 melanochrom
870	5	4.1	69	4	Q60786	Q60786 homo sapien	940	5	4.1	82	7	Q31456	Q31456 melanochrom
871	5	4.1	69	4	Q9UD5	Q9udd5 homo sapien	941	5	4.1	82	7	Q31457	Q31457 melanochrom
872	5	4.1	69	10	Q64913	Q64913 lycopersico	942	5	4.1	82	7	Q31458	Q31458 melanochrom
873	5	4.1	70	4	Q15181	Q15181 homo sapien	943	5	4.1	82	7	Q31458	Q31458 melanochrom
874	5	4.1	71	2	Q9KHU7	Q9khu7 acholeplasm	944	5	4.1	82	9	Q80090	Q80090 bacterioph
875	5	4.1	72	2	Q05230	Q05230 bacillus su	945	5	4.1	82	9	Q9MBR1	Q9mbri1 staphylococ
876	5	4.1	72	2	Q85497	Q85497 campylobact	946	5	4.1	82	9	Q9B0F3	Q9b0f3 staphylococ
877	5	4.1	72	2	Q9ALY6	Q9aly6 vibrio para	947	5	4.1	82	9	Q9B0F3	Q9b0f3 staphylococ
878	5	4.1	72	10	Q9M3P3	Q9m3p3 hordeum sec	948	5	4.1	82	12	Q91288	Q91288 human immun
879	5	4.1	73	2	Q85925	Q85925 sphingomona	949	5	4.1	82	13	Q92094	Q92094 oncorhynchu
880	5	4.1	73	5	Q21411	Q21411 caenorhabdi	950	5	4.1	82	13	Q9W7G1	Q9w7g1 oncorhynchu
881	5	4.1	73	10	Q9M5K8	Q9m5k8 zea mays (m	951	5	4.1	82	13	Q918Q0	Q918q0 oncorhynchu
882	5	4.1	73	12	Q98181	Q98181 molluscum c	952	5	4.1	82	13	Q918P9	Q918p9 oncorhynchu
883	5	4.1	74	2	Q50143	Q50143 mycobacteri	953	5	4.1	83	2	Q9CLW0	Q9clw0 pasteurella
884	5	4.1	74	2	Q84450	Q84450 chlamydia t	954	5	4.1	83	5	Q26096	Q26096 pratylenchu
885	5	4.1	74	2	Q9X6M1	Q9xm61 klebsiella	955	5	4.1	83	5	Q9U8A5	Q9u8a5 agassizea s
886	5	4.1	74	2	Q9PJU8	Q9pju8 chlamydia m	956	5	4.1	83	5	Q9S042	Q9s042 physarum po
887	5	4.1	74	2	Q9L4G8	Q9l4g8 streptococc	957	5	4.1	83	7	Q19227	Q19227 rangifer ta
888	5	4.1	74	2	Q9KCR7	Q9kcr7 bacillus ha	958	5	4.1	83	10	Q9M445	Q9m445 ciccer ariet
889	5	4.1	74	4	Q9PL93	Q9pl93 homo sapien	959	5	4.1	83	12	Q941102	Q941102 paramecium
890	5	4.1	75	2	Q9ZHF4	Q9zhf4 streptococc	960	5	4.1	84	1	Q9RND7	Q9rnd7 aeropyrum p
891	5	4.1	75	4	Q9H4S9	Q9h4s9 homo sapien	961	5	4.1	84	2	Q9KND7	Q9knd7 vibrio chol
892	5	4.1	75	5	Q96473	Q96473 plasmodium	962	5	4.1	84	3	Q9A9G1	Q9a9g1 caulobacter
893	5	4.1	75	5	Q9VIA9	Q9via9 drosophila	963	5	4.1	84	3	Q04203	Q04203 saccharomyc
894	5	4.1	75	10	Q9S860	Q9s860 pisum sativ	964	5	4.1	84	5	Q26111	Q26111 pratylenchu
895	5	4.1	75	10	Q9M688	Q9m688 gossypium h	965	5	4.1	84	10	Q65725	Q65725 brassica na
							966	5	4.1	84	12	Q72917	Q72917 hepatitis c
							967	5	4.1	84	12	Q72918	Q72918 hepatitis c
							968	5	4.1	84	12	Q72919	Q72919 hepatitis c


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DR EMBL; AE002030; AAF11467.1; -.
DR HSSP; P09097; IAB4.
DR TIGR; DR1913; -.
DR InterPro; IPR002205; DNA_topoisomIV.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00521; DNA_topoisomIV; 1.
DR SMART; SM00434; TOP4c; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 812 AA; 89824 MW; C6F8596AB57BEC00 CRC64;

Query Match          5.6%; Score 8; DB 2; Length 812;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 LEGLKAL 64
Db 377 LEGLKAL 384

RESULT 4
Q9BBP5 PRELIMINARY; PRT; 50 AA.
ID Q9BBP5
AC Q9BBP5
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE RIBOSOMAL PROTEIN L32.
GN RPL32.
OS Lotus japonicus.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Lotus.
OX NCBI_TaxID=34305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ACCESSION MG-20;
RA Kato T.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ACCESSION MG-20;
RX MEDLINE=21082929; PubMed=11214967;
RA Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
RT "Complete structure of the chloroplast genome of a legume, Lotus
RT japonicus."
RL DNA Res. 7:323-330(2000).
DR EMBL; AP002983; BAB33243.1; -.
KW Chloroplast.
SQ SEQUENCE 50 AA; 5844 MW; 5589DC533C99ECB6 CRC64;

Query Match          5.8%; Score 7; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AFSLAQS 18
Db 31 AFSLAQS 37

RESULT 5
Q9B2G1 PRELIMINARY; PRT; 98 AA.
ID Q9B2G1
AC Q9B2G1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE NADH DEHYDROGENASE SUBUNIT 4L.
GN NADH4L.
OS Isoodon macrourus (Short-nosed bandicoot).

DR EMBL; AE002030; Chordata; Craniata; Vertebrata; Euteleostomi;
DR Mammalia; Metatheria; Peramelemorphia; Peramelidae; Isoodon.
DR NCBI_TaxID=37698;
RN [1]
RP SEQUENCE FROM N.A.
RA Phillips M.J., Lin Y.-H., Harrison G.L., Penny D.;
RT "Mitochondrial Genomes of a Bandicoot and a Brush-tail Possum Confirm
RT the Monophyly of Australidelphian Marsupials."
RL Proc. R. Soc. Lond., B, Biol. Sci. 0:0-0(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Lin Y.-H., Phillips M.J.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF358864; AAK38289.1; -.
KW Mitochondrion.
SQ SEQUENCE 98 AA; 10770 MW; 69332F8F406689D4 CRC64;

Query Match          5.8%; Score 7; DB 8; Length 98;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ILAFSLA 16
Db 9 ILAFSLA 15

RESULT 6
P73929 PRELIMINARY; PRT; 143 AA.
ID P73929
AC P73929;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE HYPOTHETICAL 15.3 KDA PROTEIN.
GN SLR2101.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hikosawa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
DR EMBL; D90910; BAA17995.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 143 AA; 15349 MW; 67A2C0F7A4BBF15C CRC64;

Query Match          5.8%; Score 7; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 VPSFGIL 114
Db 75 VPSFGIL 81

RESULT 7
Q9VFR0 PRELIMINARY; PRT; 286 AA.
ID Q9VFR0
AC Q9VFR0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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CG9286 PROTEIN.
GN CG9286.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20196006; PubMed=10731132;
RX STRAIN=BERKELEY;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwee R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhargava M., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flosser C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkurov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003701; AAF54990.1; -.
DR FlyBase: FBgn0038183; CG9286.
SQ SEQUENCE 286 AA; 32212 MW; 4ADB4B95F2991CD9 CRC64;

Query Match 5.8%; Score 7; DB 5; Length 286;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 QLLQRLF 51
DB 51 QLLQRLF 57

RESULT 8
C003305 PRELIMINARY; PRT; 297 AA.
AC C003305;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS Carettochelys insculpta (pitted-shelled turtle).

Mitochondrion.
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Trionychioidea; Carettochelyidae;
OC Carettochelys.
OX NCBI_TaxID=44489;
RN [1]
RP SEQUENCE FROM N.A.
RA Shaffer H.B., Meylan P., McKnight M.L.;
RL Syst. Biol. 0:0-0(0).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: OH(2) + 2 FERRICYTOCHROME C - Q + 2
CC FERROCYTOCHROME C.
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL: U01355; AAB57646.1; -.
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00032; cytochrome_b_c; 1.
DR Pfam: PF00033; cytochrome_b_n; 1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 297
SQ SEQUENCE 297 AA; 33587 MW; EA3172420509EB1C CRC64;

Query Match 5.8%; Score 7; DB 8; Length 297;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 IMLLFTA 9
DB 91 IMLLFTA 97

RESULT 9
Q9MCB7 PRELIMINARY; PRT; 348 AA.
ID Q9MCB7
AC Q9MCB7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE MAJOR CAPSID PROTEIN.
OS Lactococcus lactis bacteriophage Q38.
OC Viruses.
OX NCBI_TaxID=100636;
RN [1]
RP SEQUENCE FROM N.A.
RA Labrie S., Moineau S.;
RT "Multiplex PCR method for the detection and the identification of
RT Lactococcal bacteriophages in cheddar cheese whey."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152411; AAF85637.1; -.
SQ SEQUENCE 348 AA; 38887 MW; 9F5C77962A7A4296 CRC64;

Query Match 5.8%; Score 7; DB 9; Length 348;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 AQSGFVAV 22
DB 273 AQSGFVAV 279

RESULT 10
Q9MCB6

CG9286 PROTEIN.
GN CG9286.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20196006; PubMed=10731132;
RX STRAIN=BERKELEY;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwee R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhargava M., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flosser C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkurov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003701; AAF54990.1; -.
DR FlyBase: FBgn0038183; CG9286.
SQ SEQUENCE 286 AA; 32212 MW; 4ADB4B95F2991CD9 CRC64;

Query Match 5.8%; Score 7; DB 5; Length 286;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 QLLQRLF 51
DB 51 QLLQRLF 57

RESULT 8
C003305 PRELIMINARY; PRT; 297 AA.
AC C003305;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS Carettochelys insculpta (pitted-shelled turtle).

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ID Q9MCB6 PRELIMINARY; PRT; 348 AA.
AC Q9MCB6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE MAJOR CAPSID PROTEIN.
OS Lactococcus lactis bacteriophage Q44.
OC Viruses.
OX NCBI_TaxID=100638;
RN [1]
RP SEQUENCE FROM N.A.
RA Labrie S., Moineau S.;
RT "Multiplex PCR method for the detection and the identification of
RL Lactococcal bacteriophages in cheddar cheese whey.";
DR Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152412; AAF85636.1; -.
SQ SEQUENCE 348 AA; 38888 MW; 112EC8EC7B512F24 CRC64;

Query Match 5.8%; Score 7; DB 9; Length 348;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 AQSEFGAV 22
Db 273 AQSEFGAV 279
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RESULT 11
Q9MCB8 PRELIMINARY; PRT; 350 AA.
ID Q9MCB8;
AC Q9MCB8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE MAJOR CAPSID PROTEIN.
OS Lactococcus lactis bacteriophage ebl.
OC Viruses.
OX NCBI_TaxID=100640;
RN [1]
RP SEQUENCE FROM N.A.
RA Labrie S., Moineau S.;
RT "Multiplex PCR method for the detection and the identification of
RL Lactococcal bacteriophages in cheddar cheese whey.";
DR Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152410; AAF85636.1; -.
SQ SEQUENCE 350 AA; 38954 MW; 552FD83845DF2960 CRC64;

Query Match 5.8%; Score 7; DB 9; Length 350;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 AQSEFGAV 22
Db 273 AQSEFGAV 279
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RESULT 12
Q9Z255 PRELIMINARY; PRT; 366 AA.
ID Q9Z255;
AC Q9Z255;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE MAJOR CAPSID PROTEIN.
OS Neurospora crassa.
OC Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE=85033713; PubMed=6238172;
RA Morelli G., Macino G.;
RT "Two intervening sequences in the ATPase subunit 6 gene of Neurospora
RT crassa. A short intron (93 base-pairs) and a long intron that is
RT stable after excision.";
RL J. Mol. Biol. 178:491-507(1984).
DR EMBL: X01075; CAA25541.1; -.
DR InterPro: IPR001982; Intron_endonuc.
DR Pfam: PF00961; Intron_maturase; 2.
KW Mitochondrion.
SQ SEQUENCE 366 AA; 42285 MW; 8AAA7BAA442BA9FA CRC64;

Query Match 5.8%; Score 7; DB 8; Length 366;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 SLEGLLK 62
Db 178 SLEGLLK 184
|||||

RESULT 13
Q9PH30 PRELIMINARY; PRT; 377 AA.
ID Q9PH30;
AC Q9PH30;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE.
GN XF0116.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.R.P., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramse E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Moon D.H., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Nhani A., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsal S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL: AE003865; AAF82929.1; -.
DR InterPro: IPR002933; Peptidase_M20.
DR Pfam: PF01546; Peptidase_M20; 1.
KW Complete proteome.
SQ SEQUENCE 377 AA; 40723 MW; 1FB7EDM4ACA2E5B8 CRC64;
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Query Match 5.8%; Score 7; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 PDLXQLL 47
 Db 363 PDLXQLL 369
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RESULT 14
 O44330 PRELIMINARY; PRT; 388 AA.
 AC O44330;
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE HEMOCYTE PROTEASE-1.
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Sphingioidea; Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jiang H., Wang Y., Kanost M.R.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
 CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
 DR EMBL; AF017663; AAB94557.1;
 DR HSP; P00750; IRTF
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Trypsin.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 388 AA; 43500 MW; C6134391EF2AE47C CRC64;

Query Match 5.8%; Score 7; DB 5; Length 388;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GGRSKR 39
 Db 39 GGRSKR 45
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RESULT 15
 Q9RVF4 PRELIMINARY; PRT; 394 AA.
 AC Q9RVF4;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE CONSERVED HYPOTHETICAL PROTEIN.
 GN DR1075.
 OS Deinococcus radiodurans.
 CC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-R1;
 RX MEDLINE-20036896; PubMed-10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,

RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1.";
 RL Science 286:1571-1577(1999).
 DR EMBL; AE001958; AAF10648.1; -.
 DR TIGR; DR1075; -.
 KW Complete proteome.
 SQ SEQUENCE 394 AA; 42220 MW; D4EE13E37BA5EABE CRC64;

Query Match 5.8%; Score 7; DB 2; Length 394;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLFTAIL 11
 Db 34 LLFTAIL 40
 |||||

Search completed: May 3, 2002, 12:32:02
 Job time: 209 sec

